

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:05:25 ; Search time 189 Seconds

(without alignments)
362.662 Million cell updates/sec

Title: US-09-770-528-2

Sequence: i MMVLSGALCFRMKDSALKVL.....IPEDPAMDAPITDFYQQCD 156

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*
9: Geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 819 | 100.0 | 156 | 2 AAW86284 | Aaw86284 Rodent in |
| 2 | 819 | 100.0 | 156 | 2 AAY28407 | Aay28407 Mouse int |
| 3 | 819 | 100.0 | 156 | 3 AAY92260 | Aay92260 Murine IL |
| 4 | 819 | 100.0 | 156 | 3 AAY45061 | Aay45061 Murine TA |
| 5 | 819 | 100.0 | 156 | 7 ABU62869 | Abu62869 Mouse sec |
| 6 | 819 | 100.0 | 156 | 8 ADJ88315 | Adj88315 Mouse int |
| 7 | 819 | 100.0 | 156 | 8 ADU04688 | Adu04688 Mouse int |
| 8 | 819 | 100.0 | 156 | 8 ADQ98213 | Adq98213 Mouse TAN |
| 9 | 814 | 99.4 | 155 | 3 AAY96937 | Aay96937 Murine IL |
| 10 | 814 | 99.4 | 155 | 4 AAB66672 | Aab66672 Invention |
| 11 | 814 | 99.4 | 155 | 4 AAB48828 | Aab48828 Murine in |
| 12 | 814 | 99.4 | 155 | 4 AAB35261 | Aab35261 Murine IL |
| 13 | 809 | 98.8 | 154 | 4 AAE06663 | Aae06663 Mouse int |
| 14 | 807 | 98.5 | 156 | 8 ADL15877 | Adl15877 Human int |
| 15 | 768 | 93.8 | 146 | 5 ABP52012 | Abp52012 NOVINTRA |
| 16 | 734 | 89.6 | 155 | 2 AAY28408 | Aay28408 Human int |
| 17 | 734 | 89.6 | 155 | 3 AAY92257 | Aay92257 Human IL- |
| 18 | 734 | 89.6 | 155 | 3 AAY45062 | Aay45062 Human TAN |
| 19 | 734 | 89.6 | 155 | 3 AAY96936 | Aay96936 Human IL- |
| 20 | 734 | 89.6 | 155 | 3 AAE06655 | Aae06655 Human int |
| 21 | 734 | 89.6 | 155 | 4 AAB66664 | Aab66664 Protein e |
| 22 | 734 | 89.6 | 155 | 4 AAB87601 | Aab87601 Human PRO |
| 23 | 734 | 89.6 | 155 | 4 AAB35262 | Aab35262 Interleuk |
| 24 | 734 | 89.6 | 155 | 4 AAB35260 | Aab35260 Human IL- |

| | | | | | |
|----|-----|------|-----|------------|---------------------|
| 25 | 734 | 89.6 | 155 | 5 ABG95926 | Abg95926 Human sec |
| 26 | 734 | 89.6 | 155 | 5 ABB84974 | Abb84974 Human PRO |
| 27 | 734 | 89.6 | 155 | 5 ABB95580 | Abb95580 Human ang |
| 28 | 734 | 89.6 | 155 | 5 ABP52018 | Abp52018 NOVINTRA |
| 29 | 734 | 89.6 | 155 | 5 ABP52034 | Abp52034 NOVINTRA |
| 30 | 734 | 89.6 | 155 | 5 ABP52047 | Abp52047 NOVINTRA |
| 31 | 734 | 89.6 | 155 | 6 ABU90951 | Abu90951 Novel hum |
| 32 | 734 | 89.6 | 155 | 6 ABO34010 | Aboc34010 Human sec |
| 33 | 734 | 89.6 | 155 | 6 ABU72027 | Abu72027 Novel hum |
| 34 | 734 | 89.6 | 155 | 6 ABP97770 | Abp97770 Amiro aci |
| 35 | 734 | 89.6 | 155 | 6 ABU71581 | Abu71581 Human sec |
| 36 | 734 | 89.6 | 155 | 6 ABU72362 | Abu72362 Human PRO |
| 37 | 734 | 89.6 | 155 | 6 ABU91035 | Abu91035 Human PRO |
| 38 | 734 | 89.6 | 155 | 6 ABO27356 | Aboc27356 Human sec |
| 39 | 734 | 89.6 | 155 | 6 ABU92551 | Abu92551 Human sec |
| 40 | 734 | 89.6 | 155 | 6 ABU81221 | Abu81221 Human sec |
| 41 | 734 | 89.6 | 155 | 6 ABO53335 | Aboc53335 Novel hum |
| 42 | 734 | 89.6 | 155 | 6 ABU98338 | Abu98338 Novel hum |
| 43 | 734 | 89.6 | 155 | 6 ABU89343 | Abu89343 Novel hum |
| 44 | 734 | 89.6 | 155 | 6 ABU82550 | Abu82550 Novel hum |
| 45 | 734 | 89.6 | 155 | 6 ABU96514 | Abu96514 Human PRO |

ALIGNMENTS

RESULT 1
AAW86284
ID AAW86284 standard; protein; 156 AA.
XX
AC AAW86284;
XX
DT 19-FEB-1999 (first entry)
XX
DE Rodent interleukin (IL)-1 delta polypeptide.
XX
KW Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;
KW inflammatory response; immune system; diagnosis; agonist; antagonist;
KW chemokine.
XX
OS Mus sp.
XX
PN W09847921-A1.
XX
PD 29-OCT-1998.
XX
PF 17-APR-1998; 98WO-US006879.
XX
PR 21-APR-1997; 97US-00837627.
PR 06-AUG-1997; 97US-0055111P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Hedrick JA, Sana TR, Bazan JF, Kastelein RA;
XX WPI, 1998-609976/51.
XX DR N-PSDB; AAV71958.
XX
PT Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g. regulating
PT the immune system and inflammatory responses.
XX
PS Claim 1; Page 89-90; 113pp; English.
XX
CC This represents a rodent interleukin (IL)-1 delta polypeptide. The
CC invention relates to a recombinant polypeptide that specifically binds
CC polyclonal antibodies (Abs) generated against a 12 consecutive amino acid
CC segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these
CC IL polypeptides are used to regulate a cell involved in an inflammatory
CC response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are
CC used to produce Abs and antigen-Ab complexes. The polypeptides, Abs and
CC the corresponding nucleic acids regulate development and/or the immune
CC system, and can be used to diagnose and treat conditions associated with
CC abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1

CC epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,
CC IL-1RA, IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1
CC epsilon polypeptides may be used as a soluble polypeptide or as a fusion
CC protein with another cytokine or chemokine

XX SQ Sequence 156 AA;

Query Match 100.0%; Score 819; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1,1e-86;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAALKVLYLHNNQILAGLHAERVIKGEISVVPNRALDASISPVIL 60
DB 1 MMVLSGALCFRMDKSAALKVLYLHNNQILAGLHAERVIKGEISVVPNRALDASISPVIL 60
QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFTRYRDMGLTSSPESAAVPGM 120
DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFTRYRDMGLTSSPESAAVPGM 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 2

AA928407
ID AAY28407 standard; protein: 156 AA.

XX AAY28407;

DT 28-SEP-1999 (first entry)

XX Mouse interleukin 1 delta.

DE Interleukin 1 delta; IL-1 delta; glaucoma; ectodermal dysplasia;

KW insulin-dependent diabetes mellitus; wrinkly skin syndrome;

KM T-cell leukemia; lymphoma; tibial muscular dystrophy.

XX OS Mus musculus.

PN W09935268-A1.

XX 15-JUL-1999.

PE 08-JAN-1999; 99WO-US000514.

PR 09-JAN-1998; 98US-0071074P.

PR 01-JUN-1998; 98US-0087393P.

PA (IMMV) IMMUNEX CORP.

PI Sims JE;

DR WPI; 1999-458310/38.

DR N-PSDB; AAX89431.

PT Murine and Human interleukin 1 delta DNA, polypeptides and its fragments,
XX useful as molecular weight markers.

PS Claim 1; Page 67; 72pp; English.

XX The present sequence represents mouse interleukin 1 delta (IL-1 delta).
CC IL-1 delta proteins are useful for the determination of the molecular
CC weight of a sample protein. The protein and its fragments are useful as
CC controls for peptide fragmentation. This is useful for determining the
CC isoelectric point of a sample protein. Antibodies generated against IL-1
CC delta and its fragmented peptides can be used to enhance the accuracy of
CC these molecular weight markers to determine the apparent molecular weight
CC and isoelectric point of a sample protein. IL-1 delta can be used to
CC screen for potential inhibitors of activity associated with IL-1 delta
CC counter-structure molecules. IL-1 delta can also be used as therapeutic
CC agents for the treatment of diseases mediated by IL-1 delta. IL-1 delta
CC may be used as a reagent in studying the interleukin 1 (IL-1) signalling

CC pathway, or as a reagent to block IL-1 signalling. The IL-1 delta coding
CC sequences can be used to identify human chromosome 2, and to identify
CC genes associated with certain diseases, especially with region 2q11-12,
CC including glaucoma, ectodermal dysplasia, insulin-dependent diabetes
CC mellitus, wrinkly skin syndrome, T-cell leukemia/ lymphoma and tibial
CC muscular dystrophy

XX SQ Sequence 156 AA;

Query Match 100.0%; Score 819; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1,1e-86;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAALKVLYLHNNQILAGLHAERVIKGEISVVPNRALDASISPVIL 60
DB 1 MMVLSGALCFRMDKSAALKVLYLHNNQILAGLHAERVIKGEISVVPNRALDASISPVIL 60
QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFTRYRDMGLTSSPESAAVPGM 120
DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFTRYRDMGLTSSPESAAVPGM 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 3

AA922260
ID AAY92260 standard; protein: 156 AA.

XX AAY92260;

DT 10-AUG-2000 (first entry)

XX Murine IL-1 homologue, zll1a3.

XX Generic; interleukin-1; IL-1; homologue; zll1a3; anti-inflammatory;

KW antagonist; pro-inflammatory; agonist; immunomodulator; antiarthritic;

KM antihemetic; osteopathic; antipsoriatic; antibacterial; cytostatic;

KW immunosuppressive; antitumor; antidiabetic; nephrotropic; vasotropic;

XX vulnerable; 2q14.

OS Mus musculus.

PN W0200020595-A1.

XX 13-APR-2000.

PE 08-OCT-1999; 99WO-US023533.

PR 08-OCT-1998; 98US-00169745.

PA (ZYMO) ZYMOGENETICS INC.

PI Shepard PO, West RR, Clegg CH;

DR WPI; 2000-303780/26.

DR N-PSDB; AAA09198.

PT Proteins useful for treatment of inflammatory conditions such as
XX new interleukin-1 homologue.

PS Example 7; Page 59-60; 64pp; English.

XX This shows an interleukin-1 (IL-1) homologue, designated zll1a3. A 350 bp
CC probe generated from the DNA sequence by PCR using AAA09199-200 was used
CC to analyze human northern blots. It is believed that zll1a3 acts through
CC IL-1 receptors. In general, zll1a3 proteins having a lys residue at
CC position 148 will have anti-inflammatory activity (e.g. AAY92256), whilst
CC those having asp (see AAY92254) or glu at this position will have pro-
CC inflammatory action. zll1a3 is used to modulate an immune response in an
CC animal (claimed). Antagonists zll1a3 forms may be used to treat or

CC prevent chronic inflammatory diseases such as rheumatoid arthritis,
 CC osteoarthritis and Lyme arthritis, psoriasis, to reduce tissue damage
 CC after ischemia, to treat septic shock, graft-versus-host disease and
 CC leukemia. The antagonists may also alleviate inflammatory bowel disease
 CC including Crohn's disease and ulcerative colitis, insulin-dependent
 CC diabetes mellitus, acute pancreatitis, glomerulonephritis and cerebral
 CC ischemia. Agonist forms of zllia3 may promote wound healing by IL-1
 CC effects on growth factor secretion and cell proliferation. They may also
 CC treat infections, especially gastrointestinal infections
 CC
 SQ Sequence 156 AA;

Query Match 100.0%; Score 819; DB 3; Length 156;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;

Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAKLVYLHNNQLAGGLHAKEYIKGEISVVPNRALDASLSPVIL 60
 DB 1 MMVLSGALCFRMDKSAKLVYLHNNQLAGGLHAKEYIKGEISVVPNRALDASLSPVIL 60
 QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFPPYRDDMGLTSSPESAAVPGW 120
 DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFPPYRDDMGLTSSPESAAVPGW 120
 QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFYQCCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFYQCCD 156

RESULT 4

AAV5061
 ID AAV45061 standard; protein; 156 AA.

AC AAV45061;

DT 31-MAY-2000 (first entry)

DE Murine TANGO-93 protein.

XX TANGO-93; cytokine; mouse; secreted protein; IL-1 expression; cancer;
 XX Interleukin-1 receptor antagonist; IL-1ra; inflammation; antiaesthetic;
 XX immunosuppressive; antirheumatic; antipsoriatic; asthma;
 XX antiinflammatory; antibacterial; antiulcer; cytostatic; immunomodulator;
 XX osteopathic; dermatological; antidiabetic; psoriasis; ulcerative colitis;
 XX graft vs-host disease; rheumatoid arthritis; inflammatory bowel disease;
 XX septic shock; cachexia; Crohn's disease; chronic myelogenous leukemia;
 XX liver disease; diabetes; osteoarthritis; Hodgkin's disease; Lyme disease;
 XX autoimmune disease; myasthenia gravis; pharmacogenomic; diagnosis;
 XX systemic lupus erythematosus; forensic; transgenic animal.

XX Mus sp.

XX MO200008045-A2.

XX 17-FEB-2000.

XX 06-AUG-1999; 99WO-US017886.

XX 07-AUG-1998; 98US-00131263.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX Pan Y;

XX WPI; 2000-205669/18.

XX N-PSDB; AAZ50811.

PT Isolated nucleic acid sequences encoding TANGO-93 polypeptide useful for
 PT treating a variety of cellular processes e.g. asthma, rheumatoid
 PT arthritis, psoriasis and autoimmune diseases.

PS Claim 9; Fig 1; 113pp; English.

CC The present sequence is the murine TANGO-93, a secreted protein, that
 CC belongs to the cytokine superfamily. It plays a role similar to secreted
 CC interleukin-1 receptor antagonist (IL-1ra) and its expression is
 CC developmentally regulated in liver, heart and bone marrow. TANGO-93
 CC modulates immune mediated inflammation and IL-1 gene or protein
 CC expression. TANGO-93 is useful as a modulating agent for regulating
 CC cellular processes like asthma, graft vs-host disease, rheumatoid
 CC arthritis, psoriasis, inflammatory bowel disease, septic shock,
 CC ulcerative colitis, Crohn's disease, chronic myelogenous leukemia,
 CC cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme disease,
 CC cachexia, and autoimmune diseases e.g. myasthenia gravis, autoimmune
 CC diabetes and systemic lupus erythematosus. Partial TANGO-93 sequences are
 CC useful in forensic biology, for diagnostic and prognostic assays,
 CC prophylactic and therapeutic treatment and pharmacogenomics. The DNA
 CC sequences are useful as hybridisation probes and primers, for isolation
 CC of TANGO-93 sequence and for the creation of transgenic animals
 CC
 SQ Sequence 156 AA;

Query Match 100.0%; Score 819; DB 3; Length 156;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;

Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAKLVYLHNNQLAGGLHAKEYIKGEISVVPNRALDASLSPVIL 60
 DB 1 MMVLSGALCFRMDKSAKLVYLHNNQLAGGLHAKEYIKGEISVVPNRALDASLSPVIL 60
 QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFPPYRDDMGLTSSPESAAVPGW 120
 DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFPPYRDDMGLTSSPESAAVPGW 120
 QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFYQCCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFYQCCD 156

RESULT 5

ABU62869
 ID ABU62869 standard; protein; 156 AA.

AC ABU62869;

DT 11-MAR-2003 (first entry)

DE Mouse secreted protein TANGO-93.

XX Mouse; TANGO-93; secreted protein; antiaesthetic; immunosuppressive;
 XX antirheumatic; antiaesthetic; antiinflammatory; antipsoriatic;
 XX cytostatic; hepatotropic; antidiabetic; dermatological; gene therapy;
 XX cytokine superfamily; asthma; graft versus-host disease; cancer;
 XX rheumatoid arthritis; psoriasis; inflammatory bowel disease;
 XX septic shock; ulcerative colitis; Crohn's disease; liver disease;
 XX chronic myelogenous leukemia; Hodgkin's disease; Lyme's disease;
 XX cachexia; autoimmune diabetes; systemic lupus erythematosus.

XX Mus musculus.

XX US2003059892-A1.

XX 27-MAR-2003.

XX 09-OCT-2002; 2002US-00267791.

XX 07-AUG-1998; 98US-00131263.

XX 06-AUG-1999; 99US-00369693.

XX (MILL-) MILLENNIUM PHARM INC.

XX Pan Y;

XX WPI; 2003-521914/49.

XX N-PSDB; ACD26633, ACD26634.

PT New TANGO-93 nucleic acid molecules and polypeptides useful for treating
 PT asthma, graft versus-host disease, rheumatoid arthritis, psoriasis,
 PT inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's
 PT disease, cancer.

XX Claim 8; Fig 1; 43pp; English.

XX The invention describes an isolated nucleic acid molecule (I) designated
 CC as TANGO-93, a secreted protein predicted to be a member of the cytokine
 CC superfamily. The polynucleotides, polypeptides compounds and methods are
 CC useful for treating asthma, graft versus-host disease, septic shock,
 CC arthritis, psoriasis, inflammatory bowel disease, ulcerative colitis,
 CC Crohn's disease, chronic myelogenous leukemia,
 CC cancer, liver disease, Hodgkin's disease, Lyme's disease, cachexia,
 CC autoimmune diabetes or systemic lupus erythematosus. This is the amino
 CC acid sequence of mouse TANGO-93

XX Sequence 156 AA;

Query Match 100.0%; Score 819; DB 7; Length 156;

Best Local Similarity 100.0%; Pred. No. 1, 1e-86;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMKDSALKVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASISPVIL 60
 DB 1 MMVLSGALCFRMKDSALKVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASISPVIL 60
 QY 61 GVGGGSQLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAVPGW 120
 DB 61 GVGGGSQLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAVPGW 120
 QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOCCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOCCD 156

RESULT 6

ADJ88315 ADJ88315 standard; protein; 156 AA.

AC ADJ88315;

DT 06-MAY-2004 (first entry)

XX Mouse interleukin-1delta protein.

XX Interleukin-1zeta; gene therapy; immune system; haematopoietic cell;

KW inflammatory disorder; infection; allergy; cancer; mouse.

XX Mus musculus.

XX US6680380-B1.

XX 20-JAN-2004.

XX 17-SRP-1999; 99US-00398412.

XX 18-SRP-1998; 98US-0100948P.

XX (SCHB) SCHERING CORP.

XX Tilmans JC;

XX WPI; 2004-189656/18.

XX New nucleic acid molecules encoding mammalian interleukin-1 polypeptides,
 PT useful for diagnosing, preventing or treating diseases associated with
 PT abnormal expression of interleukin, e.g. inflammation, infection or
 PT cancer.

XX Disclosure; SEQ ID NO 13, 36pp; English.

XX The invention relates to an isolated or recombinant nucleic acid encoding

CC interleukin-1zeta polypeptide. The invention is useful in gene therapy.

CC The composition and methods are useful in diagnosing or treating
 CC degenerative or abnormal conditions which directly or indirectly involve
 CC development, differentiation or function, e.g. of the immune system
 CC and/or haematopoietic cells. The invention may also be used for
 CC preventing or treating other diseases or disorders associated with
 CC abnormal expression or triggering of response to the interleukin, such as
 CC inflammatory disorders, infection, allergies or cancer. The present
 CC sequence is mouse interleukin-1delta.

XX Sequence 156 AA;

Query Match 100.0%; Score 819; DB 8; Length 156;

Best Local Similarity 100.0%; Pred. No. 1, 1e-86;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMKDSALKVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASISPVIL 60
 DB 1 MMVLSGALCFRMKDSALKVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASISPVIL 60
 QY 61 GVGGGSQLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAVPGW 120
 DB 61 GVGGGSQLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAVPGW 120
 QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOCCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOCCD 156

RESULT 7

AD004688 AD004688 standard; protein; 156 AA.

AC AD004688;

DT 29-JUL-2004 (first entry)

XX Mouse interleukin-1d.

XX Interleukin-1d; IL-1d; immune system; inflammatory reaction;

KW immunological disorder; mouse.

XX Mus sp.

XX Location/Qualifiers

FT Misc-difference 16 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT Misc-difference 32 /notes= "Represented by incomplete 3-letter code in

FT sequence listing"

FT Misc-difference 48 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT Misc-difference 64 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT Misc-difference 80 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT Misc-difference 96 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT Misc-difference 112 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT Misc-difference 128 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT Misc-difference 144 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT /note= "Represented by incomplete 3-letter code in

FT sequence listing"

PN US2004087766-A1.
 XX
 PD 06-MAY-2004.
 XX
 XX 27-OCT-2003; 2003US-00694978.
 PF
 XX 18-SEP-1998; 98US-0100948P.
 PR 17-SEP-1999; 99US-00398412.
 XX
 PA (TIMA/) TIMANS J C.
 XX
 XX Timans JC;
 PI
 DR WPI; 2004-374758/35.
 XX
 PT New isolated or recombinant interleukin-1 zeta polypeptide and related
 PT reagents such as antibodies, useful for treating inflammatory disease and
 PT as probes for diagnosing immunological disorders.
 XX
 PS Disclosure; SEQ ID NO 13; 42pp; English.
 XX
 CC The invention relates to interleukin-1 zeta polypeptide and
 CC polynucleotide. The agonist or antagonist of the interleukin-1 zeta is
 CC useful in modulating a cell that is involved in inflammatory response.
 CC The peptide fragments of IL-1 zeta are useful in research and diagnostic
 CC tools in the study of inflammatory reactions to antigenic challenge and
 CC the development of more effective anti-inflammatory therapeutics.
 CC Interleukin-1 zeta is useful in regulation and/or development of immune
 CC system. A polynucleotide encoding IL-1 zeta is useful for detecting the
 CC expression level of the polypeptide in a patient suspected of having an
 CC immunological disorder. The present sequence is mouse interleukin-1d.
 CC Note: The present sequence is shown in Sequence Listing and pages 6-7 of
 CC the specification. However, the sequence given in sequence listing has
 CC incomplete 3-letter codes for several amino acids.
 XX
 SQ Sequence 156 AA;
 Query Match 100.0%; Score 819; DB 8; Length 156;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMVLSGALCFRMDALKVLVYHNNQLAGLHAERKVIKGEISVVPNRALDASLSPVLL 60
 DB 1 MMVLSGALCFRMDALKVLVYHNNQLAGLHAERKVIKGEISVVPNRALDASLSPVLL 60
 QY 61 GVQGSQCCLSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSPESAAYPGW 120
 DB 61 GVQGSQCCLSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSPESAAYPGW 120
 QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
 RESULT 8
 ID ADQ98213 standard; protein; 156 AA.
 AC ADQ98213;
 DT 07-OCT-2004 (first entry)
 XX
 XX Mouse TANGO-93.
 DE
 XX mouse; TANGO-93; asthma; graft-versus-host disease; rheumatoid arthritis;
 KW psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis;
 KW Crohn's disease; chronic myelogenous leukemia; cancer; liver disease;
 KW Hodgkin's disease; osteoarthritis; Lyme disease; cachexia;
 KW autoimmune disease; myasthenia gravis; autoimmune diabetes;
 KW systemic lupus erythematosus.
 XX
 OS Mus sp.
 XX

PN US2004142420-A1.
 XX
 PD 22-JUL-2004.
 XX
 XX 12-DEC-2003; 2003US-00734985.
 PF
 XX 07-AUG-1998; 98US-00131263.
 PR 06-AUG-1999; 99US-00369693.
 PR 29-APR-2002; 2002US-00134410.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Pan Y;
 PI
 DR WPI; 2004-579909/56.
 DR N-PSDB; ADQ98212.
 XX
 PT New isolated TANGO-93 nucleic acids and proteins, useful for diagnosing,
 PT screening, or treating asthma, rheumatoid arthritis, psoriasis,
 PT inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's
 PT disease, cancer, or liver disease.
 XX
 PS Claim 8; SEQ ID NO 2; 39pp; English.
 XX
 CC The invention relates to an isolated TANGO-93 nucleic acid. The nucleic
 CC acids and polypeptides are useful for diagnosing, screening, or treating
 CC disorders having an aberrant TANGO-93 activity or expression. Diseases
 CC include asthma, graft-versus-host disease, rheumatoid arthritis,
 CC psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis,
 CC Crohn's disease, chronic myelogenous leukemia, cancer, liver disease,
 CC Hodgkin's disease, osteoarthritis, Lyme disease, cachexia, or autoimmune
 CC disease, e.g. myasthenia gravis, autoimmune diabetes, or systemic lupus
 CC erythematosus. The present sequence represents the amino acid sequence of
 CC mouse TANGO-93.
 XX
 SQ Sequence 156 AA;
 Query Match 100.0%; Score 819; DB 8; Length 156;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMVLSGALCFRMDALKVLVYHNNQLAGLHAERKVIKGEISVVPNRALDASLSPVLL 60
 DB 1 MMVLSGALCFRMDALKVLVYHNNQLAGLHAERKVIKGEISVVPNRALDASLSPVLL 60
 QY 61 GVQGSQCCLSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSPESAAYPGW 120
 DB 61 GVQGSQCCLSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSPESAAYPGW 120
 QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
 RESULT 9
 ID AAY96937 standard; protein; 155 AA.
 AC AAY96937;
 DT 31-OCT-2000 (first entry)
 XX
 XX Murine IL-1 receptor antagonist 3.
 DE
 XX mL-1RA3; interleukin-1 receptor antagonist-3; IL-1IP; osteopathic;
 KW interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
 KW anti-asthmatic; antimicrobial; respiratory; anti-ischemic; vaccine;
 KW dermatological; immunomodulatory; gastrointestinal; gene therapy.
 XX
 OS Mus sp.
 XX
 XX WO200039297-A2.
 XX

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PD 06-JUL-2000.
XX
XX 22-DEC-1999; 99WO-US030720.
XX
XX 23-DEC-1998; 98US-0113430P.
XX 22-JAN-1999; 99US-0116843P.
XX 13-APR-1999; 99US-0129122P.
XX
XX (GENENTECH INC.
XX
XX Goddard A, Pan J;
XX
XX WPI; 2000-452395/39.
XX N-PSDB; AAA51599.
XX
XX Nucleic acids encoding interleukin-1-like polypeptides, useful for
XX preventing and treating e.g. inflammation, asthma and psoriasis.
XX
XX Claim 22; Fig 9A-B; 143pp; English.
XX
XX An isolated nucleic acid molecule encoding an interleukin-1-like
XX polypeptide (IL-1 $\beta$ ) that retains one or more activities of the peptide
XX from which it is derived, such as the IL-18R binding activity of a human
XX interleukin-1 receptor antagonist-1 (IL-1Ra) polypeptide, is new. The
XX nucleic acid may be used in molecular engineering applications, e.g.
XX hybridization assays and chromosome and gene mapping studies, for
XX recombinantly producing the IL-1 $\beta$  polypeptide or for producing gene
XX knock out animals to study the role of the protein in metabolism and
XX disease processes (conversely, gene therapy protocols may be used to
XX supplement a patient's production of the polypeptide or to rectify
XX mutations that lead to the production of an active peptide). The
XX peptides produced may be used to screen for and produce modulators (e.g.
XX antibodies) of IL-1 $\beta$  protein expression and activity which may be used to
XX treat disorders associated with inappropriate IL-1 $\beta$  expression and
XX activity, such as inflammatory disorders, asthma, arthritis,
XX osteoarthritis, sepsis, acute lung injury, adult respiratory distress
XX syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
XX psoriasis, graft versus host disease and/or inflammatory bowel disease
XX
XX Sequence 155 AA;
SQ
Query Match 99.4%; Score 814; DB 3; Length 155;
Best Local Similarity 100.0%; Pred. No. 4e-86;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 MVLGALCFPMKDSALKVLYLHNNQLAGGLHAERKVIKGEISVVPNRALDASLSPVILG 61
DB 1 MVLGALCFPMKDSALKVLYLHNNQLAGGLHAERKVIKGEISVVPNRALDASLSPVILG 60
QY 62 VGGSGQCLSCGTEKGPILKLEPVNIMELYLAKESKSFYFRRDMGLTSSFESAAYPGWF 121
DB 61 VGGSGQCLSCGTEKGPILKLEPVNIMELYLAKESKSFYFRRDMGLTSSFESAAYPGWF 120
QY 122 LCTSPDADQPVRLTQIPEDPAMDAPITDFFYQOCD 156
DB 121 LCTSPDADQPVRLTQIPEDPAMDAPITDFFYQOCD 155

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XX 11-JAN-2001.
XX
XX 07-JUL-2000; 2000WO-US018710.
XX
XX 07-JUL-1999; 99US-00348942.
XX 13-OCT-1999; 99US-00417455.
XX 08-DEC-1999; 99US-00457626.
XX 10-MAR-2000; 2000US-00523552.
XX 22-MAY-2000; 2000US-00576008.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Ford J, Pace A;
XX
XX WPI; 2001-071582/08.
XX
XX Isolated nucleic acids encoding interleukin-1 (IL-1) receptor antagonist
XX proteins (referred as IL-1H1), useful in the treatment of cancer, e.g.
XX breast adenocarcinoma and brain tumors, and an inflammatory disease
XX mediated by IL-18.
XX
XX Disclosure; Page 177; 179pp; English.
XX
XX The present invention relates to interleukin (IL)-1 receptor antagonist
XX proteins. IL-1H1 is useful for treating cancer, an inflammatory disease
XX mediated by IL-18, inflammation resulting from infection or allergic
XX reactions, and inflammation associated with chronic bronchitis,
XX arthritis, diabetes or endothermia
XX
XX Sequence 155 AA;
SQ
Query Match 99.4%; Score 814; DB 4; Length 155;
Best Local Similarity 100.0%; Pred. No. 4e-86;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 MVLGALCFPMKDSALKVLYLHNNQLAGGLHAERKVIKGEISVVPNRALDASLSPVILG 61
DB 1 MVLGALCFPMKDSALKVLYLHNNQLAGGLHAERKVIKGEISVVPNRALDASLSPVILG 60
QY 62 VGGSGQCLSCGTEKGPILKLEPVNIMELYLAKESKSFYFRRDMGLTSSFESAAYPGWF 121
DB 61 VGGSGQCLSCGTEKGPILKLEPVNIMELYLAKESKSFYFRRDMGLTSSFESAAYPGWF 120
QY 122 LCTSPDADQPVRLTQIPEDPAMDAPITDFFYQOCD 156
DB 121 LCTSPDADQPVRLTQIPEDPAMDAPITDFFYQOCD 155

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RESULT 11
AAB48828
ID AAB48828 standard; protein; 155 AA.
XX
XX AAB48828;
XX
XX 09-MAR-2001 (first entry)
XX
XX Murine interleukin-1 homologue 3 (IL-1H3).
XX
XX Interleukin-1 homologue 3; IL-1H3; mouse; murine; drug screening;
XX agonist; antagonist; human disease; chronic inflammation;
XX acute inflammation; septicemia; autoimmune disease; psoriasis;
XX inflammatory bowel disease; arthritis; transplant rejection; infection;
XX graft versus host disease; acute respiratory distress syndrome; allergy;
XX asthma; restenosis; stroke; ischemia; brain injury; AIDS; bone disease;
XX osteoporosis; cancer; lymphoproliferative disorder; atherosclerosis;
XX congestive heart failure; Alzheimer's disease; immunosuppressive;
XX antimicrobial; neuroprotective.
XX
XX Mus musculus.
XX
XX WO200071583-A1.
XX

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30-NOV-2000.
 XX
 PF 24-MAY-2000; 2000MO-US014200.
 XX
 PR 24-MAY-1999; 99US-0135599P.
 PR 23-MAY-2000; 2000US-00577715.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Smith RF, Young PR, Mcdonnell PC, Halsey W;
 XX
 DR WPI; 2001-02518/03.
 DR N-PSDB; AAC81700.
 XX
 PT Murine interleukin-1 homolog polypeptide used for screening modulators of
 PT the polypeptide which can be used for treating autoimmune diseases,
 PT cancer, brain injury and bone disorders.
 XX
 PS Claim 2; Page 28-29; 31pp; English.
 XX
 CC The invention relates to murine interleukin-1 homologue 3 (IL-1H3;
 CC AAB48828) and nucleic acids which encode it (cDNA given in AAC81700).
 CC including nucleic acid sequences with at least 95% identity to AAC81700.
 CC The invention also relates to expression vectors and host cells
 CC comprising murine IL-1H3 nucleic acids, the recombinant production of
 CC murine IL-1H3, methods of screening for modulators of IL-1H3 activity,
 CC and IL-1H3 agonists and antagonists thus identified. IL-1H3 agonists and
 CC antagonists are of use for treating human diseases such as chronic or
 CC acute inflammation, septicemia, autoimmune diseases (e.g., inflammatory
 CC bowel disease, psoriasis and arthritis), transplant rejection, graft
 CC versus host disease, infection, stroke, ischemia, acute respiratory
 CC distress syndrome, allergies, asthma, restenosis, brain injury, AIDS,
 CC bone diseases (e.g., osteoporosis), cancers (e.g., lymphoproliferative
 CC disorders), congestive heart failure, atherosclerosis and Alzheimer's
 CC disease. The present sequence represents murine IL-1H3
 CC
 SQ Sequence 155 AA;
 Query Match 99.4%; Score 814; DB 4; Length 155;
 Best Local Similarity 100.0%; Pred. No. 4e-86;
 Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MVLGALCFRMDALKVLTLNHNQLAGLHAERKIKGEISVVPNALDASLSPVILG 61
 DB 1 MVLGALCFRMDALKVLTLNHNQLAGLHAERKIKGEISVVPNALDASLSPVILG 60
 QY 62 VGGGQCSCGTEKGPILKLEPVNIMELYLAKESKSTFYRRDMGLTSSPESAAVPGWF 121
 DB 61 VGGGQCSCGTEKGPILKLEPVNIMELYLAKESKSTFYRRDMGLTSSPESAAVPGWF 120
 QY 122 LCTSPEDQPVRLTQIPEDPAMDAPITDIFYQQCD 156
 DB 121 LCTSPEDQPVRLTQIPEDPAMDAPITDIFYQQCD 155
 RESULT 12
 AAB35261
 ID AAB35261 standard; protein; 155 AA.
 XX
 AC AAB35261;
 XX
 DT 08-MAY-2001 (first entry)
 XX
 DE Murine IL-1L1.
 XX
 KM Mouse; IL-1L1, interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;
 KM chromosome 2q13; inflammatory disease; heart disease; Graves' disease;
 KM rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;
 KM osteoporosis; systemic lupus erythematosus.
 XX
 OS Mus sp.
 XX

WO200105974-A2.
 XX
 PD 25-JAN-2001.
 XX
 PF 17-JUL-2000; 2000MO-US019508.
 XX
 PR 16-JUL-1999; 99US-0144298P.
 XX
 PA (INTE-) INTERLEUKIN GENETICS INC.
 XX
 PI Nicklin M, Barton J;
 XX
 DR WPI; 2001-091974/10.
 DR
 XX
 PT Nucleic acids encoding human and murine interleukin-1L1 polypeptides
 PT useful for controlling inflammatory processes.
 XX
 PS Claim 11; Fig 3; 150pp; English.
 XX
 CC The present invention provides the protein and coding sequences of the
 CC human and murine interleukin-1L1 (IL-1L1) proteins. The IL-1L1 gene is
 CC located between the IL-1beta and IL-1receptor genes at human chromosome
 CC 2q13. The sequences are useful in the diagnosis, prevention and treatment
 CC of heart disease, cancer and inflammatory diseases such as rheumatoid
 CC arthritis, systemic lupus erythematosus, inflammatory bowel disorder,
 CC diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,
 CC severe periodontal disease and pregnancy complications. The present
 CC sequence is the murine IL-1L1 protein
 CC
 SQ Sequence 155 AA;
 Query Match 99.4%; Score 814; DB 4; Length 155;
 Best Local Similarity 100.0%; Pred. No. 4e-86;
 Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MVLGALCFRMDALKVLTLNHNQLAGLHAERKIKGEISVVPNALDASLSPVILG 61
 DB 1 MVLGALCFRMDALKVLTLNHNQLAGLHAERKIKGEISVVPNALDASLSPVILG 60
 QY 62 VGGGQCSCGTEKGPILKLEPVNIMELYLAKESKSTFYRRDMGLTSSPESAAVPGWF 121
 DB 61 VGGGQCSCGTEKGPILKLEPVNIMELYLAKESKSTFYRRDMGLTSSPESAAVPGWF 120
 QY 122 LCTSPEDQPVRLTQIPEDPAMDAPITDIFYQQCD 156
 DB 121 LCTSPEDQPVRLTQIPEDPAMDAPITDIFYQQCD 155
 RESULT 13
 AAE06663
 ID AAE06663 standard; protein; 154 AA.
 XX
 AC AAE06663;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Mouse interleukin-1delta (IL-1delta) protein.
 XX
 KM Mouse; interleukin-1delta; IL-1delta; virucide; hepatotropic; fever;
 KM immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
 KM autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
 KM psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
 XX
 OS Mus sp.
 XX
 PN WO200157219-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 01-FEB-2001; 2001MO-US003285.
 XX
 PR 02-FEB-2000; 2000US-0179638P.
 XX

PA (SCHE) SCHERING CORP.

PI Debets JEMA, Timans JC, Bazan JF, Kaetelein RA;

XX WPI; 2001-488886/53.

DR Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
PT polypeptide useful for treating conditions exhibiting abnormal expression
PI of interleukin such as immunological disorders, tumor and allergy.

XX Disclosure; Fig 1; 103pp; English.

XX The invention relates to recombinant antigenic interleukin-1 like
CC molecules and their corresponding nucleic acid sequences, designated as
CC interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon). IL
CC 1delta and IL-1epsilon are useful for treating conditions exhibiting
CC abnormal expression of the interleukin such as immunological disorders,
CC tumor, inflammatory disorders, fever, hypoglycemia, psoriasis,
CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
CC HIV). The invention also relates to methods of using the composition
CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
CC utilities. IL-1delta is used as an immunogen for the production of
CC antisera or antibodies and an IL-1delta, for the interleukin or its
CC fragment. The purified interleukin is used as a reagent to detect any
CC antibodies generated in response to the presence of elevated levels of
CC expression, or immunological disorders which lead to antibody production
CC to the endogenous cytokine. The invention also contemplates the use of
CC competitive drug screening assays. The present sequence is mouse
CC interleukin-1delta (IL-1delta) protein related to the invention

SQ Sequence 154 AA;

Query Match 98.8%; Score 809; DB 4; Length 154;

Best Local Similarity 100.0%; Pred. No. 1.5e-85;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 3 VLSGALCFRMKDSALKVLYLHNNQLAGLHAKEVYIKGEISVVPNRALDASLSPVILGV 62
   |||||
DB 1 VLSGALCFRMKDSALKVLYLHNNQLAGLHAKEVYIKGEISVVPNRALDASLSPVILGV 60
   |||||
QY 63 QGSGQCLSCGTEKGPILKLEPVNIMELYLAKESKSFYRRDGLTSSFSAAYPGWL 122
   |||||
DB 61 QGSGQCLSCGTEKGPILKLEPVNIMELYLAKESKSFYRRDGLTSSFSAAYPGWL 120
   |||||
QY 123 CTSPBADQPVRLTQIPEDPAMDAPITDYPFOOCD 156
   |||||
DB 121 CTSPBADQPVRLTQIPEDPAMDAPITDYPFOOCD 154
   |||||
```

RESULT 14

ADL15877 standard; protein; 156 AA.

ADL15877;

DT 01-JUL-2004 (first entry)

DE Human interleukin-1z (IL-1z).

XX antiinflammatory; interleukin 1 zeta; IL-1 zeta; immunogen;

KW antisera production; antibody production; anti-inflammatory; human;

KW interleukin 1z; IL-1z.

OS Homo sapiens.

XX US2004068099-A1.

XX 08-APR-2004.

XX 27-OCT-2003; 2003US-00695195.

PR 18-SEP-1998; 98US-0100948P.

PR 17-SEP-1999; 99US-00398412.

XX (TIMA) TIMANS J C.

XX Timans JC;

DR WPI; 2004-304623/28.

XX Novel isolated or recombinant interleukin 1 zeta polypeptide useful as
PT immunogen for producing specific antibodies or for developing anti-
PI inflammatory therapeutics.

XX Disclosure; SEQ ID NO 13; 42pp; English.

XX The invention describes an isolated or recombinant interleukin 1 zeta
CC polypeptide (I) that specifically binds to polyclonal antibodies
CC generated against at least a 12 consecutive amino acid segment of two
CC fully defined sequences (S1) and (S2) having 218 amino acids as given in
CC the specification and comprises at least one sequence chosen from (S1)
CC and (S2). Also described are: a fusion protein comprising (I) or its
CC sequence, a detection of another cytokine or chemokine; a binding compound
CC (II) an antigen binding site from an antibody, which specifically binds
CC to (I); a composition of matter comprising a sterile polypeptide (I) or
CC to (I); (I) or (II) and a carrier such as an aqueous compound e.g., water,
CC saline and/or buffer, where the carrier is formulated for oral, rectal,
CC nasal, topical or parental administration; an isolated or recombinant
CC nucleic acid (III) that encodes (I) or several antigenic peptides of (S1)
CC or (S2); a cell (IV) transformed with (III); a method of modulating a
CC cell involved in an inflammatory response, by contacting the cell with an
CC agonist or antagonist of (I); a kit comprising a compartment of (I), (II)
CC or (III) and/or instructions for use or disposal of reagents in the kit;
CC and producing an antibody as immunogen for producing antisera or specific
CC complex. (I) is useful as immunogen for producing antisera or specific
CC antibodies or useful for developing more effective anti-inflammatory
CC therapeutics. This is the amino acid sequence of a human interleukin 1z
CC polypeptide to which the novel interleukin of the invention is related.

SQ Sequence 156 AA;

Query Match 98.5%; Score 807; DB 8; Length 156;

Best Local Similarity 98.1%; Pred. No. 2.6e-85;

Matches 153; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 MMTLSGALCFRMKDSALKVLYLHNNQLAGLHAKEVYIKGEISVVPNRALDASLSPVIL 60
   |||||
DB 1 MMTLSGALCFRMKDSALKVLYLHNNQLAGLHAKEVYIKGEISVVPNRALDASLSPVIL 60
   |||||
QY 61 GVOXGSGQCLSCGTEKGPILKLEPVNIMELYLAKESKSFYRRDGLTSSFSAAYPGW 120
   |||||
DB 61 GVOXGSGQCLSCGTEKGPILKLEPVNIMELYLAKESKSFYRRDGLTSSFSAAYPGW 120
   |||||
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDYPFOOCD 156
   |||||
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDYPFOOCD 156
   |||||
```

RESULT 15

ABP52012 standard; protein; 146 AA.

ABP52012;

DT 10-OCT-2002 (first entry)

XX NOVINTRA A homologous amino acid sequence SEQ ID NO:55.

XX Human; transmembrane protein; neuromedin protein; gonadotropin protein;

KW interleukin-1 receptor antagonist; interleukin-1 epsilon; NOVX;

KW IL-1 epsilon; IL-1 receptor antagonist; lung disease; nootropic;

KW cytosolic; neuroprotective; antiinflammatory; antibacterial;

KW immunosuppressive; cerebroprotective; antidiabetic; antithrptic;

KM antiasthmatic; anti-allergic; gene therapy; antibody-based therapy;
KM cell signalling disorder; haematopoietic disorder; endocrine; muscle;
KM neurodegenerative disorder; neurological disorder; cancer; melanoma;
KM central nervous system cancer; reproductive development disorder; asthma;
KM metabolic function disorder; bone metabolism; structure disorder; stroke;
KM inflammatory response disorder; immune regulation disorder; septic shock;
KM diabetes; arthritis; lung cancer; emphysema; allergic lung irritation;
KM lung inflammation.

OS Homo sapiens.

PN US2002068279-A1.

XX 06-JUN-2002.

PF 05-DEC-2000; 2000US-00730617.

PR 06-DEC-1999; 99US-0169056P.

PR 09-DEC-1999; 99US-0169866P.

PR 10-DEC-1999; 99US-0169866P.

PR 12-JAN-2000; 2000US-0175740P.

PA (CURA-) CURAGEN CORP.

PI Burgess C, Prayaga SK, Shimkels RA, Raetelli L, Zerhusen B;
PI Mezes P;

DR WPI; 2002-582472/62.

PT New NOVX proteins for diagnosing or treating cell signaling, immune
PT response, hematopoietic, neurodegenerative, muscle, endocrine, bone, and
PT reproductive development disorders.

PS Disclosure; Fig 10B; 110pp; English.

XX The present invention describes an isolated NOVX polypeptide, chosen from
XX human transmembrane (NOVTRAN), neuromedin (NOVNEUR), gonadotropin
XX (NOVGON), interleukin-1 (IL-1) receptor antagonist (NOVINTRA A and B),
XX and IL-1 epsilon proteins. NOVX polypeptides have nootropic, cytostatic,
XX neuroprotective, anti-inflammatory, antibacterial, immunosuppressive,
XX cerebroprotective, antidiabetic, antirheumatic, antiasthmatic and
XX anti-allergic activities, and can be used in gene therapy and antibody-
XX based therapy. NOVX polypeptides, nucleic acid (I) encoding them and an
XX antibody (III) that binds the polypeptide, are useful for treating or
XX preventing a NOVX protein-associated disorder in humans. NOVTRAN can be
XX used in the treatment of a cell signalling disorder, such as, a
XX haematopoietic disorder or a neurodegenerative disorder. NOVNEUR can be
XX used in the treatment of an endocrine, muscle, neurological disorder,
XX central nervous system cancer, breast, colon, ovarian, kidney, prostate
XX or thyroid cancer. NOVGON can be used in the treatment of a reproductive
XX development disorder, metabolic function disorder or melanoma. NOVINTRA
XX proteins can be used in the treatment of and a bone metabolism or
XX structure disorder, an inflammatory response disorder, an immune
XX regulation disorder, septic shock, stroke, diabetes, arthritis or cancer.
XX An agent which modulates the expression or activity of a human IL-1
XX epsilon protein is useful for treating a lung disease such as lung
XX cancer, asthma, emphysema, allergic lung irritation and lung inflammation
XX in a mammal. ABQ73996 to ABQ74027 and ABP51981 to ABP52048 represent
XX sequences used in the exemplification of the present invention

XX Sequence 146 AA;

Query Match 93.8%; Score 768; DB 5; Length 146;

Best Local Similarity 100.0%; Pred. No. 8.4e-81;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 CFRMDSALKVLYLHNNQLLAGLHAKEYIKGEISVVPNRALDASLSPVILGVGGSGQC 68
DB 1 CFRMDSALKVLYLHNNQLLAGLHAKEYIKGEISVVPNRALDASLSPVILGVGGSGQC 60
OY 69 LSCGTEKGPILKLEPVNIMELYGAKESKSFYYRRDMGLTSSPESAAYPGWFLCTSPRA 128

DB 61 LSCGTEKGPILKLEPVNIMELYGAKESKSFYYRRDMGLTSSPESAAYPGWFLCTSPRA 120
OY 129 DQVRLTQIPEDPAMDAPITDFFPQQ 154
DB 121 DQVRLTQIPEDPAMDAPITDFFPQQ 146

Search completed: April 5, 2006, 15:08:44
Job time : 192 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:05:57 ; Search time 23 Seconds
(without alignments)
652.601 Million cell updates/sec

Title: US-09-770-528-2
Perfect score: 819
Sequence: 1 MMTLSGALCFRMDKSLKVL.....IPEDPAMDAPITDPTFOQCD 156

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 734 | 89.6 | 155 | 2 JC7104 | interleukin-1 rece |
| 2 | 319.5 | 39.0 | 178 | 2 A44610 | interleukin-1 rece |
| 3 | 307.5 | 37.5 | 177 | 2 A30368 | interleukin-1 rece |
| 4 | 307.5 | 37.5 | 180 | 2 A39386 | interleukin-1 rece |
| 5 | 297.5 | 36.3 | 178 | 2 C40956 | interleukin-1 rece |
| 6 | 289.5 | 35.3 | 177 | 2 A54377 | interleukin-1 rece |
| 7 | 137.5 | 16.8 | 266 | 1 S23010 | interleukin-1 beta |
| 8 | 134.5 | 16.4 | 266 | 1 ICBO1B | interleukin-1 beta |
| 9 | 129 | 15.7 | 264 | 2 JN0724 | interleukin-1 beta |
| 10 | 128.5 | 15.6 | 269 | 2 JC5646 | interleukin-1 beta |
| 11 | 128 | 15.5 | 269 | 2 I55969 | interleukin-1 beta |
| 12 | 127 | 14.9 | 269 | 2 S38373 | interleukin-1 beta |
| 13 | 122 | 14.5 | 269 | 1 ICHU1B | interleukin-1 beta |
| 14 | 119 | 14.5 | 268 | 1 A30584 | interleukin-1 beta |
| 15 | 84 | 10.3 | 259 | 2 P95843 | conserved hypotet |
| 16 | 84 | 10.3 | 1427 | 2 I51669 | tumor suppressor - |
| 17 | 84 | 10.3 | 1447 | 2 A54100 | tumor suppressor p |
| 18 | 80 | 9.8 | 364 | 2 T05401 | hypothetical prote |
| 19 | 80 | 9.5 | 437 | 2 A41357 | ATP sulfurylase - |
| 20 | 78 | 9.5 | 344 | 2 A41357 | PC gamma (Igg) rec |
| 21 | 78 | 9.3 | 374 | 2 A39878 | PC gamma (Igg) rec |
| 22 | 76.5 | 9.3 | 551 | 2 C86506 | methionyl-tRNA syn |
| 23 | 76.5 | 9.3 | 551 | 2 H81552 | methionyl-tRNA syn |
| 24 | 75.5 | 9.2 | 264 | 2 A75354 | hypothetical prote |
| 25 | 75.5 | 9.2 | 1034 | 2 S36758 | mg11 protein - mou |
| 26 | 75.5 | 9.2 | 1116 | 2 T42213 | m-tomomya, isoform |
| 27 | 74 | 9.0 | 982 | 2 T19526 | hypothetical prote |
| 28 | 73.5 | 9.0 | 551 | 2 H72117 | methionine-tRNA 11 |
| 29 | 73 | 8.9 | 310 | 2 T33457 | hypothetical prote |

| | | | | | |
|----|------|-----|------|----------|----------------------|
| 30 | 73 | 8.9 | 632 | 2 T45471 | dnak-type molecule |
| 31 | 72.5 | 8.9 | 815 | 2 T36671 | probable helicase |
| 32 | 72.5 | 8.9 | 1272 | 2 S26180 | neurofascin - chic |
| 33 | 72 | 8.8 | 911 | 2 T01353 | serine/threonine p |
| 34 | 71.5 | 8.7 | 204 | 2 G97071 | folate-dependent p |
| 35 | 71.5 | 8.7 | 282 | 2 AF0902 | dihydropteroreate sy |
| 36 | 71.5 | 8.7 | 488 | 2 A87374 | hypothetical prote |
| 37 | 71.5 | 8.7 | 621 | 2 D96554 | hypothetical prote |
| 38 | 71 | 8.7 | 268 | 1 A61246 | interleukin-1 alph |
| 39 | 71 | 8.7 | 268 | 1 ICBO1A | interleukin-1 alph |
| 40 | 71 | 8.7 | 333 | 2 AH2179 | dnaf protein (limpo |
| 41 | 71 | 8.7 | 640 | 2 S37394 | dnak-type molecule |
| 42 | 70.5 | 8.6 | 550 | 2 G70597 | probable proteinase |
| 43 | 70.5 | 8.6 | 608 | 2 T05741 | dnak-type molecule |
| 44 | 70.5 | 8.6 | 663 | 2 T03581 | dnak-type molecule |
| 45 | 70.5 | 8.6 | 663 | 2 T04080 | dnak-type molecule |

ALIGNMENTS

RESULT 1
JC7104
interleukin-1 receptor antagonist - human
C/Species: Homo sapiens (man)
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: JC7104
R/Mulero, J.U.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Fort
Biochem. Biophys. Res. Commun. 263, 702-706, 1999
A/Title: IL1RH1: A novel interleukin-1 receptor antagonist gene.
A/Reference number: JC7104; MUID:9943727; PMID:10512743
A/Accession: JC7104
A/Molecule type: mRNA
A/Residues: 1-155 <MUL>
A/Cross-references: UNIPROT:Q9UBH0; UNIPARC:UPI0000034E98; GB:AF186094; NID:G6049804;
C/Genetics:
A/Gene: il1rh1
A/Map position: 2q14
C/Keywords: macrophage

Query Match 89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2.3e-67;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 MVLGALCFRMDKSLKVLINNOQLAGLNAEKYIKGBELSVVFNRLDASLPVILG 61
Db 1 MVLGALCFRMDKSLKVLINNOQLAGLNAEKYIKGBELSVVFNRLDASLPVILG 60
QY 62 VQGSQCLSCGVQEBPTLTLEPNIMELYIAKESKSFYRRDGLTSSFSBSAAYPGWF 121
Db 61 VQGSQCLSCGVQEBPTLTLEPNIMELYIAKESKSFYRRDGLTSSFSBSAAYPGWF 120
QY 122 ICTSPRADQPVRLTQIPEDPAMDAPITDPTFOQCD 156
Db 121 LCTVPEADQPVRLTQIPEDPAMDAPITDPTFOQCD 155

RESULT 2
A44610
interleukin-1 receptor antagonist precursor - mouse
N/Alternate names: IL-1Ra
C/Species: Mus musculus (house mouse)
C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C/Accession: A44610; B40956; A49031; I56106; I52970
R/Matsushima, H.; Rousset, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.
Blood 78, 616-623, 1991
A/Title: Cloning and expression of murine interleukin-1 receptor antagonist in macroph
A/Reference number: A44610; MUID:91316273; PMID:1830498
A/Accession: A44610
A/Molecule type: mRNA
A/Residues: 1-178 <MAT>
A/Cross-references: UNIPROT:P25085; UNIPARC:UPI00000041CB; GB:M64404; NID:9198296; PI
R/Bisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thomps

Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A>Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
A.Reference number: A40956; MUID:91271363; PMID:1828896
A.Accession: B40956
A.Molecule type: DNA
A.Residues: 7-178 <E1S>
A.Cross-references: UNIPARC:UPI000016CE4B; GB:M63100; NID:9198389; PIDN:AAA39310.1; PID:
R.Shuck, M.E.; Bessalun, T.E.; Tracey, D.E.; Blenkowski, M.J.
Eur. J. Immunol. 21, 2775-2780, 1991
A>Title: Cloning, heterologous expression and characterization of murine interleukin 1 r
A.Reference number: A49031; MUID:92037824; PMID:1834470
A.Accession: A49031
A.Molecule type: mRNA
A.Residues: 23-178 <SHU>
A.Cross-references: UNIPARC:UPI0000170C6C; GB:S64082; NID:9238584; PIDN:AA820265.1; PID:
A.Experimental source: peritoneal macrophages, ICR strain
A.Note: sequence extracted from NCBI backbone (NCIN:64082, NCIP:64085)
R.Zahedi, K.; Seidlin, M.F.; Rite, M.; Ezekowitz, R.B.; Whitehead, A.S.
J. Immunol. 146, 4228-4233, 1991
A>Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene mapping
A.Reference number: 156106; MUID:91250712; PMID:1828262
A.Accession: 156106
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-178 <RES>
A.Cross-references: UNIPARC:UPI00000041CB; GB:M74294; NID:9198387; PIDN:AAA39309.1; PID:
R.Zahedi, K.A.; Uhlir, C.M.; Rite, M.; Prada, A.E.; Whitehead, A.S.
Cytokine 6, 1-9, 1994
A>Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regulat
A.Reference number: 152970; MUID:94271931; PMID:8003626
A.Accession: 152970
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-178 <RE2>
A.Cross-references: UNIPARC:UPI00000041CB; GB:L32838; NID:9487864; PIDN:AAA20576.1; PID:
C.Genetics:
A.Gene: IL-1m
A.Introns: 40/2; 70/1; 107/3
C.Superfamily: interleukin-1
C.Keywords: cytokine receptor
F.1-26/Domain: signal sequence #status predicted <SIG>
F.27-178/Product: interleukin-1 receptor antagonist #status predicted <MA2>
Query Match 39.0%; Score 319.5; DB 2; Length 178;
Best Local Similarity 48.6%; Pred. No. 4.4e-25;
Matches 71; Conservative 17; Mismatches 49; Indels 9; Gaps 3;
QY 10 FRMKDSALKVLYIHNQQLAGLHAERKVIKGEISVVPNRALDASLSPVILGVQSGSOCL 69
DB 39 FRIMVNOQTFYLRNNOQLAGYLQGPNIKLEKIDVVP-----IDLHVSFLGIHGCKLCL 93
QY 70 SCCTEGPI-LKEPNIEMELVIGAKESKFTFYRRDMGLTSFESAAYPGWFLCTSPEA 128
DB 94 SCCKSGDDIKLQLEAVNITDLSNKKEDKRFTRIRSEKPTTSFESAACPGWFLCTTLEA 153
QY 129 DQPVRLTQIPEDPAMDAPITDFYFQ 154
DB 154 DRVSLTNTPEDP---LIVTKFYFQE 176

Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A>Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
A.Reference number: A40956; MUID:91271363; PMID:1828896
A.Accession: B40956
A.Molecule type: DNA
A.Residues: 7-178 <E1S>
A.Cross-references: UNIPARC:UPI000016CE4B; GB:M63100; NID:9198389; PIDN:AAA39310.1; PID:
R.Shuck, M.E.; Bessalun, T.E.; Tracey, D.E.; Blenkowski, M.J.
Eur. J. Immunol. 21, 2775-2780, 1991
A>Title: Cloning, heterologous expression and characterization of murine interleukin 1 r
A.Reference number: A49031; MUID:92037824; PMID:1834470
A.Accession: A49031
A.Molecule type: mRNA
A.Residues: 23-178 <SHU>
A.Cross-references: UNIPARC:UPI0000170C6C; GB:S64082; NID:9238584; PIDN:AA820265.1; PID:
A.Experimental source: peritoneal macrophages, ICR strain
A.Note: sequence extracted from NCBI backbone (NCIN:64082, NCIP:64085)
R.Zahedi, K.; Seidlin, M.F.; Rite, M.; Ezekowitz, R.B.; Whitehead, A.S.
J. Immunol. 146, 4228-4233, 1991
A>Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene mapping
A.Reference number: 156106; MUID:91250712; PMID:1828262
A.Accession: 156106
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-178 <RES>
A.Cross-references: UNIPARC:UPI00000041CB; GB:M74294; NID:9198387; PIDN:AAA39309.1; PID:
R.Zahedi, K.A.; Uhlir, C.M.; Rite, M.; Prada, A.E.; Whitehead, A.S.
Cytokine 6, 1-9, 1994
A>Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regulat
A.Reference number: 152970; MUID:94271931; PMID:8003626
A.Accession: 152970
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-178 <RE2>
A.Cross-references: UNIPARC:UPI00000041CB; GB:L32838; NID:9487864; PIDN:AAA20576.1; PID:
C.Genetics:
A.Gene: IL-1m
A.Introns: 40/2; 70/1; 107/3
C.Superfamily: interleukin-1
C.Keywords: cytokine receptor
F.1-26/Domain: signal sequence #status predicted <SIG>
F.27-178/Product: interleukin-1 receptor antagonist #status predicted <MA2>
Query Match 39.0%; Score 319.5; DB 2; Length 178;
Best Local Similarity 48.6%; Pred. No. 4.4e-25;
Matches 71; Conservative 17; Mismatches 49; Indels 9; Gaps 3;
QY 10 FRMKDSALKVLYIHNQQLAGLHAERKVIKGEISVVPNRALDASLSPVILGVQSGSOCL 69
DB 39 FRIMVNOQTFYLRNNOQLAGYLQGPNIKLEKIDVVP-----IDLHVSFLGIHGCKLCL 93
QY 70 SCCTEGPI-LKEPNIEMELVIGAKESKFTFYRRDMGLTSFESAAYPGWFLCTSPEA 128
DB 94 SCCKSGDDIKLQLEAVNITDLSNKKEDKRFTRIRSEKPTTSFESAACPGWFLCTTLEA 153
QY 129 DQPVRLTQIPEDPAMDAPITDFYFQ 154
DB 154 DRVSLTNTPEDP---LIVTKFYFQE 176

RESULT 4

A39386

Interleukin-1 receptor antagonist, long intracellular splice form - human
N:Contains: interleukin-1 receptor antagonist, short intracellular splice form
C:Species: Homo sapiens (man)
C>Date: 26-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C:Accession: I37893; A39386

R:Muiz, M.; Polentier, N.; Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Mantovan
J. Exp. Med. 182, 623-628, 1995

A:Title: Cloning and characterization of a new isoform of the interleukin 1 receptor ant

A:Reference number: I37893; MUID:95355865; PMID:7629520

A:Accession: I37893

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-180 <RES>

A:Cross-references: UNIPROT:P18510; UNIPARC:UPI000002ABD2; EMBL:X84348; NID:g1008970; PI
R:Haekill, S.; Martin, G.; Van Le, L.; Morris, J.; Pearce, A.; Bigler, C.F.; Jaffe, G.J.;
Proc. Natl. Acad. Sci. U.S.A. 88, 3681-3685, 1991

A:Title: CDNA cloning of an intracellular form of the human interleukin 1 receptor antag

A:Reference number: A39386; MUID:91219436; PMID:1827201

A:Accession: A39386

A:Molecule type: mRNA

A:Residues: 1-3,25-180 <HAS>

A:Cross-references: UNIPARC:UPI0000001CB5; GB:M55646; NID:g186291; PIDN:AAA59138.1; PID:
C:Comment: For an alternative splice form, see PIR:A30368

C:Genetics:

A:Gene: GDB:IL1RN

A:Cross-references: GDB:125897; OMIM:147679

A:Map position: 2q14.2-q14.2

C:Superfamily: interleukin-1

C:Keywords: alternative splicing; cytokine receptor

F:1-180/Product: interleukin-1 receptor antagonist, long intracellular splice form #stat

F:1-180/Product: interleukin-1 receptor antagonist, short intracellular splice form

Query Match 37.5%; Score 307.5; DB 2; Length 180;

Best Local Similarity 48.0%; Pred. No. 7.5e-24;

Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

10 FMKDSALKVLYLHNNQLLAGLHAKEVYKGEISVVPNRALDASLSP--VILGVQGSQ 67

41 FRIWVNOKTFYLRNNQLLAGLHAGVLOGPNVLEKIDVDP-----LEPQLFLGIHGGM 93

68 CLSC--GTEKGPILKLEPVNIMELYLAKESKSPFTFRDMDGLTSSPESAAVPGWFLCT 124

94 CLSCVSGDPTLR--LQLEAVNITDLSNNKQDKRFRFISDSGPTTSPESACPGWFLCT 151

125 SPADQPVRLTQIPEDPAMDAPITDFFYFOQ 154

152 AMEADQPVSLTNMPDE---GVMTKFPQ 178

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A/Accession: S23010
A/Molecule type: mRNA
A/Residues: 1-266 <SDO>
A/Cross-references: UNIPROT:P21621; UNIPARC:UPI0000030876; EMBL:X56972; NID:g1808; PIDN:
R/Sargan, D.R. 1992
Submitted to the EMBL Data Library, May 1992
A/Reference number: S43047
A/Accession: S43047
A/Molecule type: mRNA
A/Residues: 1-13, 'C', '15-54', 'K', '56-63', 'A', '65-144', 'L', '146-266 <SAR>
A/Cross-references: UNIPARC:UPI000016C4C5; EMBL:X54796; NID:g1273; PIDN:CAA38566.1; PID:
R/Fleckenstrand, C.; Sargan, D.
Nucleic Acids Res. 18, 7465, 1990
A/Title: Nucleotide sequence of ovine interleukin-1 beta.
A/Reference number: S13092; MUID:9108326; PMID:2263490
A/Accession: S13092
A/Molecule type: mRNA
A/Residues: 1-13, 'C', '15-54', 'K', '56-61', 'S', '63', 'A', '65-144', 'L', '146-266 <FIS>
A/Cross-references: UNIPARC:UPI0000173678; EMBL:X54796
A/Note: The authors translated the codon AGT for residue 62 as Arg
R/Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
Immunology 74, 453-460, 1991
A/Title: Molecular cloning and characterization of ovine IL-1alpha and IL-1beta.
A/Reference number: A61246; MUID:92120716; PMID:1769692
A/Accession: B61246
A/Molecule type: mRNA
A/Residues: 1-144, 'L', '146-266 <AND>
A/Cross-references: UNIPARC:UPI00002CD35
A/Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C/Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C/Genetics:
A/Gene: IL-1-beta
A/Superfamily: Interleukin-1
C/Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F/114-266/Product: interleukin-1 beta #status predicted <MAT>

Query Match          16.8%; Score 137.5; DB 1; Length 266;
Best Local Similarity 30.9%; Pred. No. 2.5e-06; Indels 17; Gaps 5;
Matches 42; Conservative 24; Mismatches 53;

QY 17 LKVLVYHNNQLLAGLHAEKVIKGEISVVPNRALDASLSPVILGVGGSGCSCGTEKG 76
DB 139 LKALHLPSQEMSRREVFVCMGFVQGEERD-----NKIPVALGIDKMLYLISC-VKKG 188
QY 77 --PIIKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAYPGWFLCTSPEDQPVRL 134
DB 189 DTPILQLEVD-PRVYPRNMEKRFVYKTEIKNTVEFESVLYENMYISTSQIERPVFL 247
QY 135 TQIPEDPAMDAPITDF 150
DB 248 GRF----RGGDDITDF 259

RESULT 8
ICBO1B
Interleukin-1 beta precursor - bovine
N/Alternate names: hematopoietin-1; IL-1 beta
C/Species: Bos primigenius taurus (catle)
C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
A/Accession: J10010; S01380
R/Malissenweil, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S.;
Mol. Immunol. 25, 429-437, 1988
A/Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin
A/Reference number: A94695; MUID:88318652; PMID:3261832
A/Accession: J10010
A/Molecule type: mRNA
A/Residues: 1-266 <MAL>
A/Cross-references: UNIPROT:P09428; UNIPARC:UPI0000167C08; GB:M37211; NID:g163200; PIDN:
R/Leong, S.R.; Plaggs, G.M.; Lawman, M.; Gray, P.W.
Nucleic Acids Res. 16, 9054, 1988
A/Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.

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A/Reference number: S01380; MUID:89016591; PMID:3262866
A/Accession: S01380
A/Molecule type: mRNA
A/Residues: 1-251, 'A', '253-266 <LEO>
A/Cross-references: UNIPARC:UPI00003086F; EMBL:X12488; NID:g448; PIDN:CAA31018.1; PID:
C/Comment: This protein is a cytokine that mediates a variety of immunoregulatory and;
C/Comment: This protein lacks a conventional signal sequence for protein export. Cleav
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C/Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-
C/Superfamily: Interleukin-1
C/Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F/114-266/Product: interleukin-1 beta #status predicted <MAT>

Query Match          16.4%; Score 134.5; DB 1; Length 266;
Best Local Similarity 30.9%; Pred. No. 5.1e-06; Indels 17; Gaps 5;
Matches 42; Conservative 23; Mismatches 54;

QY 17 LKVLVYHNNQLLAGLHAEKVIKGEISVVPNRALDASLSPVILGVGGSGCSCGTEKG 76
DB 139 LKALHLPSQEMSRREVFVCMGFVQGEERD-----NKIPVALGIDKMLYLISC-VKKG 188
QY 77 --PIIKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAYPGWFLCTSPEDQPVRL 134
DB 189 DTPILQLEVD-PRVYPRNMEKRFVYKTEIKNTVEFESVLYENMYISTSQIERPVFL 247
QY 135 TQIPEDPAMDAPITDF 150
DB 248 GRF----RGGDDITDF 259

RESULT 9
UN0724
Interleukin-1 beta precursor - pig
N/Alternate names: hematopoietin-1; IL-1 beta
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
A/Accession: JN0724
R/Hueher, M.J.; Lin, G.; Smith, D.M.; Murrugh, M.P.; Molitor, T.W.
Gene 129, 285-289, 1993
A/Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1
A/Reference number: JN0724; MUID:93314975; PMID:8325511
A/Accession: JN0724
A/Molecule type: mRNA
A/Residues: 1-267 <HUE>
A/Cross-references: UNIPROT:P26889; UNIPARC:UPI000030879; GB:M86725; NID:g164607; PI:
A/Experimental source: alveolar macrophage
C/Comment: This protein is a pleiotropic cytokine that mediates a variety of processe
C/Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C/Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin
C/Superfamily: Interleukin-1
C/Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrop
F/115-267/Product: interleukin-1 beta #status predicted <IL1>
F/77/Binding site: myristate (lys) (covalent) #status predicted

Query Match          15.8%; Score 129; DB 1; Length 267;
Best Local Similarity 29.9%; Pred. No. 1.9e-05; Indels 36; Gaps 8;
Matches 47; Conservative 26; Mismatches 48;

QY 2 MVLGALCFPMKDSALKVLYLHNNQLLAGLHAEK-----IKGEISVVPNRALDASLS 56
DB 132 LVYLA-----PHMLKALH-----LLTGDLKEVFVCMGFVQGDSDN-----NKI 170
QY 57 PVILGVGGSGCSC-CTEKGPIIKLEPVNIMELYGAKESKSFYRRDMGLTSSPESA 115
DB 171 PVTLGIGKMLYLSVCMKMDTPILQLEDID-PRVYPRNMEKRFVYKTEIKNTVEFESA 229
QY 116 AYPGWFLCTSPEDQPVRL--TQIPEDPAMDAPITDF 150
DB 230 LYENMYISTSQIERPVFLGNSKGRD-----ITDF 260

RESULT 10

```


GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:05:45 ; Search time 230 Seconds

(without alignments)
478,532 Million cell updates/sec

Title: US-09-770-528-2

Perfect score: 819
Sequence: 1 MMVLGALGCRMDALKVL.....IPEDPAWDAPITPFQOCD 156

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80-+*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the chance being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------------|--------------------|
| 1 | 819 | 100.0 | 156 | 1 IL1F5_MOUSE | Q9GY1 mus musculu |
| 2 | 734 | 89.6 | 155 | 1 IL1F5_HUMAN | Q9UBD h interluek |
| 3 | 319.5 | 39.0 | 159 | 2 Q542M1_MOUSE | Q542M1 mus musculu |
| 4 | 319.5 | 39.0 | 178 | 1 IL1RA_MOUSE | P25085 mus musculu |
| 5 | 319.5 | 39.0 | 178 | 2 Q542C7_MOUSE | Q542C7 mus musculu |
| 6 | 317.5 | 38.8 | 159 | 2 Q8CGAL_MOUSE | Q8CGAL mus musculu |
| 7 | 312 | 38.1 | 152 | 1 IL1RA_MOUSE | Q8439 mus musculu |
| 8 | 309 | 37.7 | 152 | 2 Q56AT8_HUMAN | Q56AT8 homo sapien |
| 9 | 307.5 | 37.5 | 177 | 1 IL1RA_HUMAN | P18510 homo sapien |
| 10 | 307.5 | 37.5 | 180 | 2 Q53SC2_HUMAN | Q53SC2 homo sapien |
| 11 | 305.5 | 37.3 | 177 | 1 IL1RA_MACFA | Q77771 macaca fasc |
| 12 | 305.5 | 37.3 | 177 | 1 IL1RA_TURTR | Q86M24 macaca fasc |
| 13 | 304 | 37.1 | 152 | 1 IL1RA_HUMAN | Q8W41 homo sapien |
| 14 | 304 | 37.1 | 152 | 2 Q53SR9_HUMAN | Q53SR9 homo sapien |
| 15 | 301.5 | 36.8 | 174 | 1 IL1RA_BOVIN | Q77482 bos taurus |
| 16 | 299.5 | 36.6 | 177 | 1 IL1RA_PIG | Q29086 sus scrofa |
| 17 | 297.5 | 36.3 | 178 | 1 IL1RA_RAT | P25086 rattus norv |
| 18 | 289.5 | 35.3 | 177 | 1 IL1RA_CANFA | P26890 cynctolagus |
| 19 | 285.5 | 34.9 | 176 | 1 IL1RA_CANFA | Q9BEH0 canis famli |
| 20 | 269.5 | 32.9 | 177 | 1 IL1RA_HORSE | O18999 equus cabal |
| 21 | 213.5 | 26.1 | 82 | 2 Q6PUJ3_PIG | Q6PUJ3 sus scrofa |
| 22 | 190.5 | 23.3 | 72 | 2 Q77771_HORSE | Q77771 equus cabal |
| 23 | 189.5 | 23.1 | 218 | 1 IL1F7_HUMAN | Q9NZ6 homo sapien |
| 24 | 184.5 | 22.5 | 138 | 2 Q4R3X2_HUMAN | Q4R3X2 macaca fasc |
| 25 | 182.5 | 22.3 | 219 | 2 Q7RU00_HUMAN | Q7RU00 homo sapien |
| 26 | 181.5 | 22.2 | 160 | 1 IL1F6_MOUSE | Q9J12 mus musculu |
| 27 | 169.5 | 20.7 | 267 | 2 Q73909_CHICK | Q73909 gallus gall |
| 28 | 167.5 | 20.5 | 158 | 1 IL1F6_HUMAN | Q9UB4 homo sapien |
| 29 | 167.5 | 20.5 | 158 | 2 Q5BLR4_HUMAN | Q5BL4 homo sapien |
| 30 | 167.5 | 20.5 | 158 | 2 Q53SR7_HUMAN | Q53S7 homo sapien |
| 31 | 165.5 | 20.2 | 183 | 1 IL1F8_MOUSE | Q9d66 mus musculu |

ALIGNMENTS

| RESULT 1 | IL1F5_MOUSE | STANDARD; | PRT; | 156 AA. |
|----------|--|-----------|------|---------|
| AC | Q9GY1; Q9JG2; | | | |
| DT | 28-FEB-2003 (Rel. 41, Last sequence update) | | | |
| DT | 13-SEP-2005 (Rel. 48, Last annotation update) | | | |
| DE | Interleukin 1 family member 5 (IL-1F5) (Interleukin-1 delta) (IL-1H1) (Interleukin-1-like protein 1) (IL-1L1) (Interleukin-1 H1) | | | |
| DE | (IL-1H1) (Interleukin-1 homolog 3) (IL-1H3). | | | |
| GN | Name=IL1F5; Synonyms=Fl1d, Il1h3, Il1h1; | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; | | | |
| OX | Muroidea; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| OX | [1] | | | |
| RP | NUCLEOTIDE SEQUENCE. | | | |
| RX | MEDLINE=21359532; PubMed=11466363; | | | |
| RA | Debeers R., Timans J.C., Homay B., Zurawski S., Sana T.R., Lo S., | | | |
| RA | Wagner J., Edwards G., Clifford T., Menon S., Bazan J.P., | | | |
| RA | Kastlein R.A.; | | | |
| RT | "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function | | | |
| RT | as an antagonist and agonist of NF-kappa B activation through the | | | |
| RT | Orphan IL-1 receptor-related protein 2"; | | | |
| RL | J. Immunol. 167:1440-1446(2001). | | | |
| RL | [2] | | | |
| RP | NUCLEOTIDE SEQUENCE. | | | |
| RX | MEDLINE=20545212; PubMed=11093146; | | | |
| RA | DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMU3299>3.0.CO;2-S; | | | |
| RA | Barton J.L., Herbst R., Boesio D., Higgins L., Nicklin M.J.H.; | | | |
| RT | "A tissue specific IL-1 receptor antagonist homolog from the IL-1 | | | |
| RT | cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities"; | | | |
| RL | Eur. J. Immunol. 30:3299-3308(2000). | | | |
| RL | [3] | | | |
| RP | NUCLEOTIDE SEQUENCE. | | | |
| RX | MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308; | | | |
| RA | Kumar S., McDonnell P.C., Lehr R., Tierney L., Timans M.N., | | | |
| RA | Griewold D.E., Capper E.A., Tai-Singer R., Wells G.I., Doyle M.L., | | | |
| RA | Young P.R.; | | | |
| RT | "Identification and initial characterization of four novel members of | | | |
| RT | the interleukin-1 family"; | | | |
| RL | J. Biol. Chem. 275:10308-10314(2000). | | | |
| RL | [4] | | | |
| RP | NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]. | | | |
| RC | STRAIN=C57BL/6J; TISSUE=Stomach; and Tongue; | | | |
| RX | MEDLINE=22554683; PubMed=12466851; DOI=10.1038/nature01266; | | | |
| RA | Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., | | | |
| RA | Nikado T., Otsu N., Saito R., Suzuki H., Yamakawa I., Kiyosawa H., | | | |
| RA | Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., | | | |
| RA | Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., | | | |
| RA | Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., | | | |
| RA | Blake J.A., Brad T., Brusic V., Chochia C., Corbani L.E., Cousins S., | | | |
| RA | Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., | | | |

| | | | | | |
|----|-------|------|-----|----------------|--------------------|
| 32 | 157 | 19.2 | 169 | 1 IL1F9_HUMAN | Q9NZ8 homo sapien |
| 33 | 157 | 19.2 | 169 | 2 Q56B91_HUMAN | Q56B91 homo sapien |
| 34 | 155 | 18.9 | 290 | 2 Q712K7_ORNAN | Q712K7 ornithorhyn |
| 35 | 148.5 | 18.1 | 246 | 2 Q98SG5_SCOPX | Q98SG5 scopithalmu |
| 36 | 145 | 17.7 | 253 | 2 Q5K4R2_GADMO | Q5K4R2 gadus morhu |
| 37 | 143 | 17.5 | 283 | 2 Q71JM3_XENLA | Q71JM3 xenopus lae |
| 38 | 143 | 17.5 | 283 | 2 Q9PVZ5_XENLA | Q9PVZ5 xenopus lae |
| 39 | 143 | 17.5 | 286 | 2 Q569Q8_XENLA | Q569Q8 xenopus lae |
| 40 | 137.5 | 16.8 | 266 | 1 IL1B_SHEEP | Q21621 ovis aries |
| 41 | 137 | 16.7 | 268 | 1 IL1B_HORSE | Q28386 equus cabal |
| 42 | 136.5 | 16.7 | 266 | 1 IL1B_CEREL | P51745 cervus elap |
| 43 | 135.5 | 16.5 | 266 | 2 Q5R458_BUBBU | Q5R458 bubalus bub |
| 44 | 134.5 | 16.4 | 266 | 1 IL1B_BOVIN | P09428 bos taurus |
| 45 | 132 | 16.1 | 247 | 2 Q8QGW0_PAROL | Q8QGW0 paratichthy |

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 GRIMMOND S., Guecinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 KANAI A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
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 NAGASHIMA T., Nunata K., Okido T., Pavan W.J., Perte G., Pesole G.,
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 RAVASI T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
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 VERAARDO R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 WILMING L.G., Wyshaw-Borle A., Yanagisawa M., Yang I., Yang L.,
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 BIRNEY E., Hayashizaki Y.,
 "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 Nature 420:563-573 (2002).
 [5]
 X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 3-156, AND DISULFIDE BOND.
 PUBMED:12974628; DOI=10.1021/bi0341197;
 Dunn E.F., Gay N.J., Bristow A.F., Gearing D.P., O'Neill L.A.J.,
 RA "High-resolution structure of murine interleukin 1 homologue IL-1F5
 reveals unique loop conformations for receptor binding specificity."
 Biochemistry 42:10938-10944 (2003).
 CC -1- FUNCTION: Is a highly and a specific antagonist of the IL-1
 receptor-related protein 2-mediated response to interleukin 1
 signaling system analogous to interleukin-1 alpha (IL-1A), beta
 (IL-1B) receptor agonist and interleukin-1 receptor type I (IL-
 1RI), that is present in epithelial barriers and takes part in
 local inflammatory response (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: Highly abundant in embryonic tissue and
 tissues containing epithelial cells.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 DR EMBL, AF230378, AAF91275.1; -; mRNA.
 DR EMBL, AK009741, BAB26471.1; -; mRNA.
 DR EMBL, AK008977, BAB26002.1; -; mRNA.
 DR EMBL, AJ250429, CAB59831.1; ALT_INT; mRNA.
 DR EMBL, AF200495, AAF69251.1; -; mRNA.
 DR PDB, 1MD6, X-ray; A=3-156.
 DR Ensembl, ENSMUSG0000026983, Mus musculus.
 DR MGI, MGI:1859325, Il1f5.
 DR InterPro, IPR000975, Interleukin 1.
 DR InterPro, IPR003296, InterleukinIL1B.
 DR InterPro, IPR003297, InterleukinIL1RA.
 DR PANTHER, PTHR10078:SF2, InterleukinIL1RA, 1.
 DR Pfam, PF00340, IL1, 1.
 DR PRINTS, PR00264, INTERLEUKIN1.
 DR PRINTS, PR01359, INTERLEUKIN1B.
 DR PRINTS, PR01360, INTERLEUKIN1X.
 DR ProDom, PD002536, Interleukin_1, 1.
 DR SMART, SM00125, IL1, 1.
 DR PROSITE, PS00253, INTERLEUKIN_1, 1.
 DR 3D-structure, Cytokine; Multigene family.
 FT DISULFID 9 155
 FT CONFLICT 2 2 Missing (in Ref. 3).
 SO SEQUENCE 156 AA; 17136 MW; A4D1BE2F93CF77A7 CRC64;
 Query Match 100.0%; Score 819; DB 1; Length 156;

Best Local Similarity 100.0%; Pred. No. 7,6e-77;
 Matches 156; Conservative 0; Mismatch 0; Indels 0; Gaps 0;
 QY 1 MMTLSGALCFRMDASLKVLYTHNNQLAGLHAERYIKGEISVVPNRALDASLSPVIL 60
 DB 1 MMTLSGALCFRMDASLKVLYTHNNQLAGLHAERYIKGEISVVPNRALDASLSPVIL 60
 QY 61 GVGQGGSCGLSCGTEKGPILKLEPVNIMELYLGAKESESFFPYRDMGLTSSFESAAYPGW 120
 DB 61 GVGQGGSCGLSCGTEKGPILKLEPVNIMELYLGAKESESFFPYRDMGLTSSFESAAYPGW 120
 QY 121 FLCTSPADQPVRLTQPEDPADAPITDFYFOQCD 156
 DB 121 FLCTSPADQPVRLTQPEDPADAPITDFYFOQCD 156
 RESULT 2
 IL1F5 HUMAN STANDARD; PRT; 155 AA.
 AC Q9UBH0; Q56AT9; Q7RTZ6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Interleukin 1 family member 5 (IL-1F5) (interleukin-1 delta) (IL-1
 delta) (PIL1 delta) (interleukin-1-like protein 1) (IL-1L1)
 DE (interleukin-1 H1) (IL-1H1) (interleukin-1 receptor antagonist
 DE homolog 1) (IL-1ra homolog 1) (IL-1 related protein 3) (IL-1RP3).
 GN Name=IL1F5; Synonyms=PIL1D, IL1H1, IL1L1, IL1RP3;
 GN ORFNames=UNQ1896/PRO4342;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 OX [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Placenta;
 RX MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
 RA Smith D.E., Renshaw B.R., Ketchum R.R., Kudin M., Garika K.E.,
 RA Sims J.E.;
 RT "Four new members expand the IL-1 superfamily.";
 RL J. Biol. Chem. 275:1169-1175 (2000).
 [2]
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP TISSUE=Fetal skin;
 RX MEDLINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440;
 RA Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
 RA Drmanac R., Ford J.E.;
 RT "IL1H1: a novel interleukin-1 receptor antagonist gene.";
 RL Biochem. Biophys. Res. Commun. 263:702-706 (1999).
 [3]
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP TISSUE=Placenta;
 RX MEDLINE=20545212; PubMed=11093146;
 RA Barton J.L., Herbst R., Bosisto D., Higgins L., Nicklin M.J.H.;
 RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1
 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
 RL Eur. J. Immunol. 30:3299-3308 (2000).
 [4]
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP MEDLINE=21359532; PubMed=11466363;
 RA Debets R., Timans G.C., Honey B., Zurawski S., Sana T.R., Lo S.,
 RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
 RA Kastalein R.A.;
 RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
 as an antagonist and agonist of NF-kappa B activation through the
 orphan IL-1 receptor-related protein 2.";
 RL J. Immunol. 167:1440-1446 (2001).
 [5]
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RP MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184;
 RA Bustfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,

RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.,
 RT "Identification and gene organization of three novel members of the
 RT IL-1 family on human chromosome 2." ;
 RL Genomics 66:213-216(2000).
 [6]
 RA NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
 RA Micklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
 RA Kornman K.;
 RT "A sequence-based map of the nine genes of the human interleukin-1
 RT cluster." ;
 RL Genomics 79:718-725(2002).
 [7]
 RA NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eason D., Foster J.S., Grimaldi C., Gu O., Hase P.E., Heidens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liso D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
 RA Sehagiri S., Simmons L., Singh U., Smith V., Stinson J., Vagts A.,
 RA Vandena R.L., Watanabe C., Weand D., Woods K., Xie M.-H.,
 RA Yausua D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment." ;
 RL Genome Res. 13:2265-2270(2003).
 [8]
 RA NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT SER-47.
 RA Rieder M.J., Johanson E.J., da Ponte S.H., Haefliger N.C., Ahern M.O.,
 RA Bertucci C.B., Wong M.W., Yi Q., Nickerson D.A.;
 RT "SeattleSNP: NHLBI H66682 program for genomic applications, UW-
 RT FRCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>)."
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 [9]
 RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15815621; DOI=10.1038/nature03466;
 RA Hillier L.W., Graves T.A., Fulton R.S., Fulton L.A., Pepin K.H.,
 RA Minx P., Wagner-McPherson C., Layman D., Wyllie K., Sekhon M.,
 RA Becker M.C., Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E.,
 RA Krentitz C., Oddy L., Du H., Sun H., Bradshaw-Cordum H., Ali J.,
 RA Carter J., Cordes M., Harris A., Isak A., van Brunt A., Nguyen C.,
 RA Du P., Courtney L., Kalicki J., Ozersky P., Abbott S., Armstrong J.,
 RA Belter E.A., Caruso L., Cedroni M., Cotton M., Davidson T., Desai A.,
 RA Elliott G., Erb T., Fronick C., Gaige T., Haakenson W., Haglund K.,
 RA Holmes A., Harkins R., Kim K., Kruchowski S.S., Strong C.M.,
 RA Grewal N., Goyes E., Hou S., Levy A., Martinka S., Mead K.,
 RA McLellan M.D., Meyer R., Randall-Maher J., Tomlinson C.,
 RA Dauphin-Kohlberg S., Kozlowski-Reilly A., Shan N.,
 RA Leonard S., Pearson C., Trani L., Radionenko M., Waligorski J.E.,
 RA Wang C., Rock S.M., Tin-Wollam A.-M., Maupin R., Latreille P.,
 RA Wendl M.C., Yang S.-P., Pohl C., Wallis J.W., Spilch J., Bieri T.A.,
 RA Berkowicz N., Nelson J.O., Osborne J., Ding L., Meyer R., Sabo A.,
 RA Shorland Y., Simha P., Woldmann P.E., Cook K.L., Hickenbotham M.T.,
 RA Eldred J., Williams D., Jones T.A., She X., Ciccarelli F.D.,
 RA Izaurrealde E., Taylor J., Schmutz J., Myers R.M., Cox D.R., Huang X.,
 RA McPherson J.D., Mardis E.R., Clifton S.W., Warren W.C.,
 RA Chinwalla A.T., Eddy S.R., Marra M.A., Ovcharenko I., Furey T.S.,
 RA Miller W., Richter E.E., Bork P., Suyama M., Torrents D.,
 RA Waterston R.H., Wilson R.K.;
 RT "Generation and annotation of the DNA sequences of human chromosomes 2
 RT and 4." ;
 RL Nature 434:724-731(2005).
 [10]
 RA NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX TISSUE=Placenta; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Deje J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Datchenko I., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Pirange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boeak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy M., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smilins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: is a highly and a specific antagonist of the IL-1
 CC receptor-related protein 2-mediated response to interleukin 1
 CC family member 9 (IL1F9). Could constitute part of an independent
 CC signaling system analogous to interleukin-1 alpha (IL-1A), beta
 CC (IL-1B) receptor agonist and interleukin-1 receptor type I (IL-
 CC 1RI), that is present in epithelial barriers and takes part in
 CC local inflammatory response.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Predominantly expressed in keratinocytes but
 CC not in fibroblasts, endothelial cells or melanocytes. Detected
 CC also in the spleen, brain leukocyte and macrophage cell types.
 CC -1- INDUCTION: By phorbol ester (PMA) and lipopolysaccharide (LPS)
 CC treatment in macrophage cell line.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
 CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AF201830; AAF25210.1; -; mRNA.
 CC EMBL: AF186094; AAF02757.1; -; mRNA.
 CC EMBL: AJ242737; CAB59822.1; -; mRNA.
 CC EMBL: AJ242738; CAB59823.1; -; mRNA.
 CC EMBL: AJ271338; CAB67704.1; -; Genomic DNA.
 CC EMBL: AF216693; AAF76581.1; -; Genomic DNA.
 CC EMBL: AF230377; AAF91274.1; -; mRNA.
 CC EMBL: BN000002; CAD29877.1; -; Genomic DNA.
 CC EMBL: AY359117; AAO89475.1; -; mRNA.
 CC EMBL: AY972853; AAX59031.1; -; Genomic DNA.
 CC EMBL: AC016724; AAY14990.1; -; Genomic DNA.
 CC EMBL: BC024747; AAH24747.1; -; mRNA.
 CC PIR: JC7104; JC7104.
 CC HSSP: P18510; IILR.
 CC SWR: O9UBH0; 2-155.
 CC IntAct: O9UBH0; -
 CC Ensembl: ENSG00000136695; Homo sapiens.
 CC HNC: HNC:15561; IILF5.
 CC MIM: 605507; -
 CC CO: GO:0005157; F:interleukin-1 receptor antagonist activity; TAS.
 CC InterPro: IPR000975; Interleukin_1.
 CC InterPro: IPR003296; InterleukinIL1B.
 CC InterPro: IPR003297; InterleukinIL1RA.
 CC PANTHER: PTHR10078:SF2; InterleukinIL1RA; 1.
 CC Pfam: PF00340; IL1; 1.
 CC PRINTS: PR00264; INTERLEUKIN1.
 CC PRINTS: PR01359; INTERLEUKIN1B.
 CC PRINTS: PR01360; INTERLEUKIN1X.
 CC ProDom: PD002536; Interleukin_1; 1.
 CC SMART: SM00125; IL1; 1.
 CC PROSITE: PS00253; INTERLEUKIN_1; 1.
 CC KX Cytokine; Multigene family; Polymorphism.
 CC DISUFID By similarity.
 CC VARIANT 8 154 N -> S.
 CC VARIANT 47 47

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Query Match      89.6%; Score 734; DB 1; Length 155;
Best Local Similarity 91.0%; Pred. No. 5.2e-68;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 MYLSCALCFRMDKSLKVLVYHNNOLLAGLHAERYIGEEISVYPNRLDASLSPVILG 61
DB 1 MYLSCALCFRMDKSLKVLVYHNNOLLAGLHAERYIGEEISVYPNRLDASLSPVILG 60
QY 62 VGGGSCGSCSGVGGVGGTTLLEPVNIMELTGAKESKSPFYRRDGLTSSPESAAYPGMF 121
DB 61 VGGGSCGSCSGVGGVGGTTLLEPVNIMELTGAKESKSPFYRRDGLTSSPESAAYPGMF 120
QY 122 LCTSPADQVRLTQIPEDPADAPITDYPFOCCD 156
DB 121 LCTSPADQVRLTQIPEDPADAPITDYPFOCCD 155

RESULT 3
0542M1_MOUSE PRELIMINARY; PRT; 159 AA.
ID 0542M1_MOUSE PRELIMINARY; PRT; 159 AA.
AC 0542M1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE 0 day neonate skin cDNA, RIKEN full-length enriched library,
DE clone:4632427H7 product:interleukin 1 receptor antagonist, full
DE insert sequence.
OS Name=Illm;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murine; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner J., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barth G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Noraki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszewski A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Otsu N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,
RA Yagi K., Tomaru R., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad D., Brusic V., Chothia C., Corpani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Girimonte S., Gustincich S., Hirokawa N., Jackson I.D., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanagawa A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Saito T., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vetraro R., Wagner L., Walshtedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszewski A., Yangiwa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kondo H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Naki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,
RA Yaunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kondo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kondo H., Akiyama J., Nishi K., Kiyosawa H., Nishino T., Harada A.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujitake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384 format
RT sequencing pipeline with 384 multicapillary sequencer.";
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kondo H., Konda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yaunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK076296; BAC36291.1; -; mRNA.
DR MGI; MGI:96547; Illrn.
DR GO; GO:0030073; P:insulin secretion; IMP.
DR GO; GO:0006629; P:lipid metabolism; IMP.
KW Receptor.
SQ
Sequence 159 AA; 17995 MW; A7CD35D137846222 CRO64;

Query Match      39.0%; Score 319.5; DB 2; Length 159;
Best Local Similarity 48.6%; Pred. No. 7e-25;
Matches 71; Conservative 17; Mismatches 49; Indels 9; Gaps 3;

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QY 10 FRKMSALKLYLHNNOLLAGLHAKEVYKGEISVYPRALDASLSPVLGVGSSQCL 69
 DB 20 FRMDWNTQKTYFLRNNOIAGVLOGPNIKLEBKIDWP-----IDLHSPVFGHGGKCL 74
 QY 70 SCGTEKGP1-LKLEPVNIMELYLAKESKSFYFRDMGLTSSPESAAYPGWFLCTSPBA 128
 DB 75 SCAGSGDITQLEBVENITDLSKNEEDKRTFTFRSEKPTTSPESAACPGWFLCTTLEA 134
 QY 129 DQPVRLTQIPEDPAMPADITDFYPOQ 154
 DB 135 DRPVSLTNTPEEP---LIVTKFYFOE 157
 RESULT 4
 IL1RA MOUSE
 ID IL1RA MOUSE STANDARD; PRT; 178 AA.
 AC P25085; 070207;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (IRAP)
 DE (IL1 inhibitor) (IL-1RN).
 GN Name=Il1rn; Synonyms=Il-1ra;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
 RX MEDLINE=91250712; PubMed=1828262;
 RA Zahedi K., Seiden M.F., Rits M., Ezekowitz R.A., Whitehead A.S.;
 RT "Mouse IL-1 receptor antagonist protein. Molecular characterization,
 RT gene mapping, and expression of mRNA in vitro and in vivo.";
 RL J. Immunol. 146:4228-4233(1991).
 RN [2]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
 RX MEDLINE=91316273; PubMed=1830498;
 RA Matsushima H., Roussel M.F., Matsushima K., Hishinuma A., Sherr C.J.;
 RT "Cloning and expression of murine interleukin-1 receptor antagonist in
 RT macrophages stimulated by colony-stimulating factor 1.";
 RL Blood 78:616-623(1991).
 RN [3]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
 RX STRAIN=Swiss;
 RA MEDLINE=94271931; PubMed=8003626; DOI=10.1016/1043-4666(94)90001-9;
 RA Zahedi K.A., Uhlar C.M., Rits M., Prada A.E., Whitehead A.S.;
 RT "The mouse interleukin 1 receptor antagonist protein: gene structure
 RT and regulation in vitro.";
 RL Cytokine 6:1-9(1994).
 RN [4]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
 RX STRAIN=FVB X DBA/1 LACJ;
 RA MEDLINE=98209757; PubMed=9550387;
 RA Gabay C., Porter B., Pantuzzi G., Arend W.P.;
 RT "Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning
 RT and protein expression of intracellular isoform and tissue
 RT distribution of secreted and intracellular IL-1 receptor antagonist in
 RT vivo.";
 RL J. Immunol. 159:5905-5913(1997).
 RN [5]
 RP NUCLEOTIDE SEQUENCE OF 7-178.
 RX MEDLINE=91271363; PubMed=1828896;
 RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
 RA Brandhuber B.J., Thompson R.C.;
 RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
 RT gene family: evolution of a cytokine control mechanism.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
 RN [6]
 RP NUCLEOTIDE SEQUENCE OF 23-178.
 RX MEDLINE=92037844; PubMed=1834470;
 RA Shuck M.E., Bessatsu T.E., Tracey D.E., Bienkowski M.J.;
 RT "Cloning, heterologous expression and characterization of murine

RT Interleukin 1 receptor antagonist protein.";
 RL Eur. J. Immunol. 21:2775-2780(1991).
 CC -1- FUNCTION: Inhibits the activity of IL-1 by binding to its
 CC receptor. Has no IL-1 like activity.
 CC -1- SUBCELLULAR LOCATION: Secreted (isoform 1). Cytoplasmic (isoform
 CC 2).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P25085-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P25085-2; Sequence=VSP 002652;
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC
 CC This Swiss-Prot entry is copyrigh. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; M74294; AAA9309.1; -; mRNA.
 CC EMBL; M64404; AAA9277.1; -; mRNA.
 CC EMBL; U32838; AAA30576.1; -; Genomic_DNA.
 CC EMBL; AF001795; AAC15251.1; -; mRNA.
 CC EMBL; M57525; AAA9278.1; -; mRNA.
 CC EMBL; M63100; AAA9310.1; -; Genomic_DNA.
 CC EMBL; S64082; AAB20265.1; -; mRNA.
 CC PIR; A44610; A44610.
 CC HSSP; P18510; 11RA.
 CC SMR; P25085; 35-178.
 CC EMBL; ENSMUSG0000026981; Mus musculus.
 CC MGI; MGI:96547; Il1rn.
 CC GO; GO:0030073; P:insulin secretion; IMP.
 CC GO; GO:0006629; P:lipid metabolism; IMP.
 CC InterPro; IPR000975; Interleukin_1.
 CC InterPro; IPR003286; InterleukinIL1B.
 CC InterPro; IPR003287; InterleukinIL1RA.
 CC PANTHER; PTHR10078:SP2; InterleukinIL1RA; 1.
 CC Pfam; PF00340; IL1; 1.
 CC PRINTS; PR00264; INTERLEUKIN1.
 CC PRINTS; PR01359; INTERLEUKIN1B.
 CC PRINTS; PR01360; INTERLEUKIN1X.
 CC ProDom; PD002536; Interleukin_1; 1.
 CC PROSITE; PS00253; INTERLEUKIN_1; 1.
 CC K1 Alternative splicing; Glycoprotein; Signal.
 CC SIGNAL 1 26 By similarity.
 CC CHAIN 27 178 Interleukin-1 receptor antagonist
 CC protein.
 CC CARBOHYD 110 110 N-linked (GlcNAc...) (potential).
 CC DISULFD 92 142 By similarity.
 CC VARSPIC 1 21 MEICWGPYSHISLILILFFH -> MA (in isoform
 CC 2).
 CC
 CC SEQUENCE 178 AA; 20274 MW; 84AA002A119C024 CRC64;
 Query Match 39.0%; Score 319.5; DB 1; Length 178;
 Best Local Similarity 48.6%; Pred. No. 8e-25;
 Matches 71; Conservative 17; Mismatches 49; Indels 9; Gaps 3;
 QY 10 FRKMSALKLYLHNNOLLAGLHAKEVYKGEISVYPRALDASLSPVLGVGSSQCL 69
 DB 39 FRMDWNTQKTYFLRNNOIAGVLOGPNIKLEBKIDWP-----IDLHSPVFGHGGKCL 93
 QY 70 SCGTEKGP1-LKLEPVNIMELYLAKESKSFYFRDMGLTSSPESAAYPGWFLCTSPBA 128
 DB 94 SCAGSGDITQLEBVENITDLSKNEEDKRTFTFRSEKPTTSPESAACPGWFLCTTLEA 153
 QY 129 DQPVRLTQIPEDPAMPADITDFYPOQ 154
 DB 154 DRPVSLTNTPEEP---LIVTKFYFOE 176
 RESULT 5

Q542C7_MOUSE PRELIMINARY; PRT; 178 AA.
 ID Q542C7_MOUSE PRELIMINARY; PRT; 178 AA.
 AC Q542C7_MOUSE PRELIMINARY; PRT; 178 AA.
 DT 13-SEP-2005 (TREMblrel. 31, Created)
 DT 13-SEP-2005 (TREMblrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMblrel. 31, Last annotation update)
 DE NOD-derived CD11c+ve dendritic cells cDNA, RIKEN full-length enriched
 DE full insert sequence.
 GN Name:ilrn;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; PubMed=11217851; DOI=10.1038/35055500;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota T., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
 RA Fieschmann W., Gaasterland T., Gissi C., King B., Kozliwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
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 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,
 RA Brownstein M. J., Bull C., Hofmann M., Hume D. A., Kamiya M., Lee N. H.,
 RA Guelincklin M. J., Hill D., Hofmann M., Hume D. A., Kamiya M., Lee N. H.,
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Monbaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K. H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohatsu S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; PubMed=12466851; DOI=10.1038/nature01266;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi T., Bono H., Kondo S.,
 RA Nikaide I., Otsu N., Saito R., Suzuki H., Yamana K. I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojohori T.,
 RA Baldarelli R., Hill D. P., Bull C., Hume D. A., Quackenbush J.,
 RA Schriml L. M., Kanapin A., Matsuda H., Batalov S., Beisel K. W.,
 RA Blake J. A., Brad T., Bruscia V., Fletcher C., Godzik A., Gough J.,
 RA Dala E., Dargatzis T. A., Fletcher C. F., Forrest A., Frazer K. S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Jarvis E. D.,
 RA Grimmond S., Guscinich S., Hirokawa N., Jackson I. J., Jarvis E. D.,
 RA Kani A., Kawai H., Kawasawa Y., Kedzierski R. M., King B. L.,
 RA Kani A., Kawai H., Kawasawa Y., Lee Y., Lenhard B., Lyons P. A.,
 RA Maglott D. R., Maltas L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W. J., Perle G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J. V., Qi D., Kamachandran S.,
 RA Ravasi T., Reed J. C., Reed D. J., Reid J., Ring B. Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C. A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M. S., Teasdale R. D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanebe Y., Wells C.,
 RA Wilming L. G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavoian M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kondo H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Maki K., Kawai J., Aizawa K., Aizawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

MIYAZAKI A., SAKAI K., SASAKI D., SHIBATA K., SHINAGAWA A.,
 YASUNISHI A., YOSHINO M., WATERSTON R., LANDER E. S., ROGERS J.,
 BIRNEY E., HAYASHIZAKI Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; PubMed=11042159; DOI=10.1101/gr.145100;
 RX MEDLINE=20530913; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
 RA Kondo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 [5]
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DT 01-MAR-2003 (Tremblrel. 23, last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, last annotation update)
DE Interleukin 1 receptor antagonist.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC Virgin mouse. Taken by biopsy.
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Stachenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uebli T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lomellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gutarrae P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Harte S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
RA Scherach A., Schrein J.B., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC Virgin mouse. Taken by biopsy.
RL Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC042532; AAH42532.1; -, mRNA.
DR HSSP; P18510; 11LR.
DR SMR; Q8CGA1; 16-159.
DR MGI; MGI:96547; 11LR.
DR GO; GO:0030073; P:insulin secretion; IMP.
DR GO; GO:0006629; P:lipid metabolism; IMP.
DR InterPro; IPR003294; InterleukinIL1B.
DR InterPro; IPR003296; InterleukinIL1B.
DR InterPro; IPR003297; InterleukinIL1RA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR PRINTS; PR01359; INTERLEUKIN1B.
DR PRINTS; PR01360; INTERLEUKIN1X.
DR PRINTS; PR01357; INTERLEUKIN1A.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR Receptor.
SQ SEQUENCE 159 AA; 17995 MW; BCA081C17290367 CRC64;
Query Match 38.8%; Score 317.5; DB 2; Length 159;
Best Local Similarity 47.9%; Pred. No. 1,1e-24;
Matches 70; Conservative 18; Mismatches 49; Indels 9; Gaps 3;
QY 10 FFMKDSALVLYLHNNQLAGGLHAKEVKIGEEISVPPNRALDASISPVILGVGSSGCL 69
DB 20 FFIWDTNQKTFYLRNNQLAGVLYQGPNIKLEKLDVDP-----IDLHSAFLGIHGKCL 74
QY 70 SCGTGKGPL-LKLEPYNIMELYGAKESKSFYPRDMDGLTSFESAAPGWFCLCTSPRA 128

DB 75 SCAGSDDIKQLQLEENITDLSKKEEDKRFPIINSEKPTTSFESAACPGWFLCTTLEA 134
QY 129 DQPVRLTQIPBDPAMDAPITDFYFQ 154
DB 135 DRPVSLTNRPEP---LIVTKFYFQ 157
RESULT 7
ID IL1FA MOUSE STANDARD; PRT; 152 AA.
AC 08R459;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin 1 family member 10 (IL-1F10).
GN Name=IL1F10;
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Swiss Webster / NIH;
RX MEDLINE=21988051; PubMed=11991723; DOI=10.1006/geno.2002.6752;
RX Taylor S.L., Renshaw B.R., Garika R.E., Smith D.E., Sims J.E.,
RT "Genomic organization of the interleukin-1 locus.";
RL Genomics 79:726-733(2002).
CC -1- FUNCTION: Binds soluble IL-1 receptor type 1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (by similarity).
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AY071844; AAL67155.1; -, mRNA.
DR HSSP; P18510; 11RA.
DR Ensemble; ENSMUSG0000046845; Mus musculus.
DR MGI; MGI:2652548; 11F10.
DR InterPro; IPR000975; Interleukin_1.
DR InterPro; IPR003296; InterleukinIL1B.
DR InterPro; IPR003297; InterleukinIL1RA.
DR PANTHER; PTHR10078:SP2; InterleukinIL1RA; 1.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR PRINTS; PR01359; INTERLEUKIN1B.
DR PRINTS; PR01360; INTERLEUKIN1X.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; FALSE_NEG.
KW Cytokine; Multigene family.
SQ SEQUENCE 152 AA; 17078 MW; 9AD03EB0C36C1D8A CRC64;
Query Match 38.1%; Score 312; DB 1; Length 152;
Best Local Similarity 43.5%; Pred. No. 4e-24;
Matches 67; Conservative 28; Mismatches 53; Indels 6; Gaps 3;
QY 1 MMTLSGALCFRMKDSALVLYLHNNQLAGGLHAKEVKIGEEISVPPNRALDASISPVIL 60
DB 1 MCSLPMARYYIIKDHQALYTRNQLLGPDSDN-YSPEKVCILPFRGIDRSKVPFL 59
QY 61 GVOGSSGCLSC-GTEKGPLIKLEPYNIMELYGAKESKSFYPRDMDGLTSFESAAYPG 119
DB 60 GMVGSSCCLACVKTREGPLQLQEDVNIEDLYKGEQITRFTFQNSLDSAPRLDAACPG 119
QY 120 WFLCTSPADQPVRLTQIPBDPAMDAPITDFYFQ 153
DB 120 WFLGPAEPQGPVQVTKESF---PSTHTETVYFE 149

RESULT 8
Q56AT8 HUMAN PRELIMINARY; PRT; 152 AA.
AC OS6AT8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Interleukin 1 family, member 10 (Theta).
GN Name=IL1F10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homindaee;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Rieder M.J., Johanson E.J., da Ponte S.H., Haetings N.C., Ahern M.O.,
RA Betts C.B., Wong M.W., Yi O., Nickerson D.A.;
RL Submitted (MAR-2005) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY972854; AAK59032.1; -; Genomic DNA.
SQ SEQUENCE 152 AA; 16975 MW; DF9735100FC711B2 CRC64;
Query March 37.7%; Score 309; DB 2; Length 152;
Best Local Similarity 45.2%; Pred. No. 8.1e-24;
Matches 70; Conservative 23; Mismatches 56; Indels 6; Gaps 3;
QY 1 MMTLSGALCFRMKDSALKVLYAHNNQLAGLHAERVKGEISVVPNPAUDASLPYL 60
DB 1 MSLIMARYIITKVDQKALYTRDQGLVGPDPVANNCC-AEKICTLPNKGIDRTKVPITL 59
QY 61 GVQGSQCLSC-GTEGPIILKLEPVNIMELYGAKESFTFYRRDMGLTSSFESAAYPG 119
DB 60 GIGQSGRCACVETGSPSLQEDVIEILYKGEATFTFFQSSSGSAFLKAAAMPG 119
QY 120 WFLCTSPADQVRLTQIPEDPAMPADPTDFYFQQ 154
DB 120 WFLCGAPQPPQVQLTKSEPSA---RTKRYFEQ 150
RESULT 9
IL1RA HUMAN STANDARD; PRT; 177 AA.
ID IL1RA HUMAN
AC P18510; Q14628; Q7RTZ4; Q96GP6; Q9UPC0;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (IRAP)
DE (IL1 inhibitor) (IL-1RN) (ICIL-1RA).
GN Name=IL1RN; Synonyms=IL1F3, IL1RA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homindaee;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=90220867; PubMed=2139180; DOI=10.1038/344633a0;
RA Carter D.B., Delbel M.R., Jr., Dunn C.J., Tomich C.S.C., Laborde A.L.,
RA Slighcom J.L., Berger A.E., Bienkowski M.J., Sun F.F., McEwan R.N.,
RA Harris P.K.W., Yem A.W., Waszak G.A., Chosay J.G., Siu L.C.,
RA Hardee M.M., Zurcher-Nelly H.A., Reardon I.M., Heinrichson R.L.,
RA Triesdale S.E., Shelly J.A., Bessalu T.E., Taylor B.M., Tracey D.E.;
RT "Purification, cloning, expression and biological characterization of
an interleukin-1 receptor antagonist protein.";
RL Nature 344:633-638 (1990).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=90136921; PubMed=2137201; DOI=10.1038/343341a0;
RA Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T.,
RA Hannum C.H., Thompson R.C.;
RT "Primary structure and functional expression from complementary DNA of
a human interleukin-1 receptor antagonist.";
RL Nature 343:341-346 (1990).

[3]
RN NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=91271363; PubMed=1828896;
RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA Brandhuber B.J., Thompson R.C.;
RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
gene family: evolution of a cytokine control mechanism.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236 (1991).
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=92338323; PubMed=1385987; DOI=10.1016/1043-4666(92)90041-O;
RA Leonard A., Gorman P., Carrier M., Griffiths S., Courtney H., Sheer D.,
RA Solari R.;
RT "Cloning and chromosome mapping of the human interleukin-1 receptor
antagonist gene.";
RL Cytokine 4:83-89 (1992).
RN [5]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 3).
RX MEDLINE=97146044; PubMed=892991;
RA Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slighcom J.L.,
RA Arend W.P., Smith M.F., Jr.;
RT "Intracellular IL-1 receptor antagonist promoter: cell type-specific
and inducible regulatory regions.";
RL J. Immunol. 158:748-755 (1997).
RN [6]
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RX MEDLINE=91219436; PubMed=1827201;
RA Haekil S., Martin G., van Le L., Morris J., Peace A., Bigler C.F.,
RA Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.;
RT "cDNA cloning of an intracellular form of the human interleukin 1
receptor antagonist associated with epithelium.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685 (1991).
RN [7]
RP NUCLEOTIDE SEQUENCE (ISOFORM 3).
RX MEDLINE=9535865; PubMed=7629520; DOI=10.1084/jem.182.2.623;
RA Muzio M., Polentarutti N., Sironi M., Poli G., De Giola L.,
RA Introna M., Mantovani A., Colotta F.;
RT "Cloning and characterization of a new isoform of the interleukin 1
receptor antagonist.";
RL J. Exp. Med. 182:623-628 (1995).
RN [8]
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RA Rieder M.J., Carrington D.P., Haetings N.C., Ahern M.O.,
RA Kulane S.A., Rajkumar N., Toch B.J., Yi O., Nickerson D.A.;
RT "Sequences of the NHLBI HL66682 program for genomic applications, UN-
FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>)."
RL Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.
RN [9]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM 2).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Udell T.B., Tothiyuk S., Carninci P., Pirange C.,
RA Bask S.S., McGowan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Bohak S., Mowley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,
RA Richards S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Valley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skalska U., Smallus D.E.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [10]
RP PROTEIN SEQUENCE OF 26-45, AND CARBOHYDRATE-LINKAGE SITE ASN-109.

RX MEDLINE=90136920; PubMed=2137200; DOI=10.1038/343336a0;
 RA Hannon C.H., Wilcox C.J., Arad W.P., Joslin F.G., DiPpe D.J.,
 RA Helmdal P.L., Ames L.G., Sommer A., Eisenberg S.P., Thompson R.C.;
 RT "Interleukin-1 receptor antagonist activity of a human interleukin-1
 RT inhibitor.";
 RL Nature 343:336-340(1990).
 RN [11]
 RP PROTEIN SEQUENCE OF 26-52
 RX MEDLINE=90354444; PubMed=2143761;
 RA Binkowski M.J., Bessalu T.E., Berger A.E., Truesdell S.E.,
 RA Shelly J.A., Laborde A.L., Zurcher-Neely H.A., Reardon I.M.,
 RA Henriksen R.L., Chosay J.G., Tracey D.E.;
 RT "Purification and characterization of interleukin 1 receptor level
 RT antagonist proteins from THP-1 cells.";
 RL J. Biol. Chem. 265:14505-14511(1990).
 RN [12]
 RP NUCLEOTIDE SEQUENCE OF 35-177 (ISOFORM 4).
 RX MEDLINE=98183404; PubMed=951884; DOI=10.1006/bbrc.1998.8217;
 RA Weisbach L., Tran K., Colquhoun S.A., Champliand M.F., Towle C.A.;
 RT "Detection of an interleukin-1 intracellular receptor antagonist mRNA
 RT variant.";
 RL Biochem. Biophys. Res. Commun. 244:91-95(1998).
 RN [13]
 RP IDENTIFICATION OF ISOFORM 2.
 RX MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
 RA Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald W.G., Duff W.G.,
 RA Korman M.J.;
 RT "A sequence-based map of the nine genes of the human interleukin-1
 RT cluster.";
 RL Genomics 79:718-725(2002).
 RN [14]
 RP STRUCTURE BY NMR.
 RX MEDLINE=92297633; PubMed=1534997;
 RA Stockman B.U., Scallil T.A., Roy M., Ulrich E.L., Strakalatis N.A.,
 RA Brunner D.P., Yem A.W., Deibel M.R., Jr.;
 RT "Secondary structure and topology of interleukin-1 receptor antagonist
 RT protein determined by heteronuclear three-dimensional NMR
 RT spectroscopy.";
 RL Biochemistry 31:5237-5244(1992).
 RN [15]
 RP STRUCTURE BY NMR.
 RX MEDLINE=94320651; PubMed=8045306; DOI=10.1016/0014-5793(94)00643-1;
 RA Stockman B.U., Scallil T.A., Strakalatis N.A., Brunner D.P.,
 RA Yem A.W., Deibel M.R., Jr.;
 RT "Solution structure of human interleukin-1 receptor antagonist
 RT protein.";
 RL FEBS Lett. 349:79-83(1994).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=94230369; PubMed=8175703;
 RA Vigers G.P.A., Caffes P., Evans R.J., Thompson R.C., Eisenberg S.P.,
 RA Brandhuber B.J.;
 RT "X-ray structure of interleukin-1 receptor antagonist at 2.0-A
 RT resolution.";
 RL J. Biol. Chem. 269:12874-12879(1994).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE=95172072; PubMed=7867645;
 RA Schreuder H.A., Rondenau J.-M., Tardif C., Soffientini A., Sarubbi E.,
 RA Akesson A., Bowlin T.L., Yanofsky S., Barrett R.W.;
 RT "Refined crystal structure of the interleukin-1 receptor antagonist.
 RT Presence of a disulfide link and a cis-proline.";
 RL Eur. J. Biochem. 227:838-847(1995).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH IL1R.
 RX MEDLINE=97215904; PubMed=9062194;
 RA Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A., Sarubbi E.,
 RA Sarubbi E., Akesson A., Bowlin T., Yanofsky S., Barrett R.W.;
 RT "A new cytokine-receptor binding mode revealed by the crystal
 RT structure of the IL-1 receptor with an antagonist.";
 RL Nature 386:194-200(1997).
 CC -1- FUNCTION: Inhibits the activity of IL-1 by binding to its
 CC receptor. Has no IL-1 like activity.

```
CC -1- SUBCELLULAR LOCATION: Secreted (Isoform 1). Cytoplasmic (isoforms
CC 2, 3 and 4)
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=P18510-1; Sequence=Displayed;
CC Name=2; Synonyms=ICIL-1ra;
CC IsoId=P18510-2; Sequence=VSP_002649;
CC Name=3; Synonyms=ICIL-1ra type II;
CC IsoId=P18510-3; Sequence=VSP_002650;
CC Name=4;
CC IsoId=P18510-4; Sequence=VSP_002651;
CC -1- TISSUE SPECIFICITY: The intracellular form of IL1RN is
CC predominantly expressed in epithelial cells.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC -1- DATABASE: NAME-R&D Systems' cyclohex source book: IL1RN;
CC WWW="http://www.rndsys.com/asp/g_slebuilder.asp?bodyid=205".
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QY 10 FMKOSALKVLYIHNNQLLAGLHAERKVIKGEISVFNRLDASLSP--VILGVGGSG 67
 DB 38 FRIMVNOCKTFYLRNNQLVAGYLGENTKLEEKIDVVP-----IEPAMFLGIHGKXL 90
 QY 68 CISCGETKGPILK--LEPNIIMELVIGAESEKSFYTRRDMGLTSSFEAAIPGWFICTS 125
 DB 91 CIAC-VKSGDEIKLGLPEPNITLTLNNSKEDKRFARIRSDSGPTTSSFEACPGWFLCTA 149
 QY 126 PEADQPVRLTQIPEDPAMDAPITDFYFQQ 154
 DB 150 LETDQVGLTNPQDA---VQYTKFIFQQ 175

RESULT 13
 IL1FA HUMAN
 ID IL1FA HUMAN STANDARD: PRT; 152 AA.
 AC Q8MWZ1, Q7RTZ5, Q969H5, Q9BIX1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 13-SEP-2003 (Rel. 48, Last sequence update)
 DT 13-SEP-2003 (Rel. 48, Last annotation update)
 DE Interleukin-1 family member 10 (IL-1F10) (Interleukin-1 receptor
 antagonist-like FcR11 theta) (Interleukin-1 theta) (IL-1 theta) (F111
 theta) (Interleukin-1 HT2) (IL-1HT2).
 GN Name=IL1F10; Synonyms=F111T, IL1HT2;
 OS ORFNames=FKSG75, UNO6119/PRO20041;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
 RC TISSUE=Thymus;
 RX MEDLINE=21615180; PubMed=11747621; DOI=10.1089/107999001753289505;
 RA Benen J.T., Dawson P.A., Mychaleckyj J.C., Bowden D.W.;
 RT "Identification of a novel human cytokine gene in the interleukin gene
 cluster on chromosome 2q12-14.";
 RL J. Interferon Cytokine Res. 21:899-904 (2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
 RA Wang Y.-G., Li T., Gong L.;
 RT "Identification and characterization of FKSG75, a novel member of the
 interleukin-1 family.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA / mRNA) (ISOFORM 1), AND VARIANTS
 RP THR-44 AND ASP-51.
 RC TISSUE=Fetal skin;
 RX MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200;
 RA Lin H., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussell J.,
 RA Phee A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;
 RT "Cloning and characterization of IL1HT2, a novel interleukin-1 family
 member.";
 RL J. Biol. Chem. 276:20597-20602 (2001).
 RN [4]
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
 RX MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
 RA Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
 RA Kornman K.;
 RT "A sequence-based map of the nine genes of the human interleukin-1
 cluster.";
 RL Genomics 79:718-725 (2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM 1).
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Adaya E., Baker K., Baldwin D.T., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Heidens S.,
 RA Huang A., Kim H.S., Klimowaki L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
 RA Sehnaghi S., Simmons L., Singh J., Smith V., Stinson O., Vagts A.,
 RA Vandlen R.L., Watanabe C., Wleand D., Woode K., Xie M.-H.,

RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 effort to identify novel human secreted and transmembrane proteins: a
 bioinformatics assessment.";
 RL Genome Res. 13:2265-2270 (2003).
 RN [6]
 RP VARIANTS THR-44 AND ASP-51.
 RX MEDLINE=21988051; PubMed=11991723; DOI=10.1006/geno.2002.6752;
 RA Taylor S.L., Renshaw B.R., Garika K.E., Smith D.E., Sims J.E.;
 RT "Genomic organization of the interleukin-1 locus.";
 RL Genomics 79:726-733 (2002).
 CC -1- FUNCTION: Binds soluble IL-1 receptor type 1.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8MWZ1-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8MWZ1-2; Sequence=VSP_002658;
 CC Note=No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Expressed in fetal skin, spleen and tonsil.
 CC Expressed mostly in the basal epithelia of skin and in
 CC proliferating B cells of the tonsil.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL: AY029413; AAK33010.1; -; mRNA.
 DR EMBL: AY026753; AAK01948.1; -; mRNA.
 DR EMBL: AF334755; AAK68048.1; -; mRNA.
 DR EMBL: AF334756; AAK68049.1; -; Genomic DNA.
 DR EMBL: BN000002; CAD29878.1; -; Genomic DNA.
 DR EMBL: AY358846; AAO89205.1; -; mRNA.
 DR HSSP: P18510; IL1R.
 DR Ensembl: ENSG00000136697; Homo sapiens.
 DR HGNC: HGNC:15552; IL1F10.
 DR InterPro: IPR000975; Interleukin-1.
 DR InterPro: IPR003296; InterleukinF1b.
 DR InterPro: IPR003297; InterleukinIL1RA.
 DR PANTHER: PTHR10078:SF2; InterleukinIL1RA; 1.
 DR Pfam: PF00340; IL1; 1.
 DR PRINTS: PRO0264; INTERLEUKIN1.
 DR PRINTS: PRO1359; INTRLEUKIN1B.
 DR PRINTS: PRO1360; INTRLEUKIN1X.
 DR PRODOM: PD002536; Interleukin_1; 1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; FALSE NEG.
 KM Alternative splicing; Cytokine, Multigene family; Polymorphism.
 FT YIIKIVADQKALYTRDQGLVDDPVADNCC -> MSSSPL
 FT VASPSPLC 9
 FT PEPIDPAKSLQHGVPISLSDSSLSLL (in isoform 2).
 FT /FtId=VSP_002658.
 FT VARIANT 44 44 I -> T (in dbSNP: 6761276).
 FT /FtId=VAR_014262.
 FT VARIANT 51 51 A -> D (in dbSNP: 6743376).
 FT /FtId=VAR_014263.
 SQ SEQUENCE 152 AA; 16943 MW; E0ABD2496551B34F CRC64;

Query Match 37.1%; Score 304; DB 1; Length 152;
 Best Local Similarity 44.5%; Pred. No. 2,7e-23;
 Matches 69; Conservative 24; Mismatches 56; Indels 6; Gaps 3;

QY 1 MMTVIGALCFRMKOSALKVLYIHNNQLLAGLHAERKVIKGEISVFNRLDASLSPYIL 60
 DB 1 MCSLPMARYIYIKADPKALYTRDQGLVDDPVADNCC-ABKICILPNRGIARXKVPFIFL 59
 QY 61 GYGGSGCASC-GTEKGPILKLEPNVIMELVIGAESEKSFYTRRDMGLTSSFEAAIPG 119
 DB 60 GIGGSGRCACVETBSPSLQLEVDNVEILYIKGEISVFNRLDASLSPYIL 119

QY 120 WFLCTSPADQPVRLTQIPEDPAMDAPITDFYFOO 154
 Db 120 WFLCGPAEPQOPVQLTKESEPSA-----RTKFFYFQ 150

RESULT 14

Q53SR9 HUMAN PRELIMINARY; PRT; 152 AA.
 ID Q53SR9_HUMAN
 AC Q53SR9;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Hypothetical protein IL1F10.
 GN Name=IL1F10;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homiidae;
 OC Homo.
 OC NCBI_Taxid=9606;
 OX NCBI [1]

RN NUCLEOTIDE SEQUENCE.
 RA Armstrong J., Haekenson W.;
 RT "The sequence of Homo sapiens BAC clone RP11-339F22."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RA NUCLEOTIDE SEQUENCE.
 RA Waterston R.H.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RA NUCLEOTIDE SEQUENCE.
 RA Waterston R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RA NUCLEOTIDE SEQUENCE.
 RA Wilson R.K.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC016724; AA1491.1; -; Genomic DNA.
 KW Hypothetical protein.
 SO SEQUENCE 152 AA; 16943 MW; E0ABD2496551B34F CRC64;

Query Match 37.1%; Score 304; DB 2; Length 152;
 Best Local Similarity 44.5%; Pred. No. 2,7e-23;
 Matches 69; Conservative 24; Mismatches 56; Indels 6; Gaps 3;

QY 1 MMTLSGALCFRMDKSAIKVLYLHNNQLAGLHAEKVIKGEISVFNRLADSLSPVIL 60
 Db 1 MCGSLPMARYIYIKYADQKALYTRDQLVGDPLVADNCC-AKICILPNRGLATKVPIL 59
 QY 61 GVGGSGSCISC-GTEKGPILKLEPVNIMELYLAKESKSPFFYRRDMGLTSSPESAAYPG 119
 Db 60 GIGGSSRCCLACVETEEGSLQLEBDVNIJELTKGSEKATRTFFQSSSGSARLDAAMPG 119
 QY 120 WFLCTSPADQPVRLTQIPEDPAMDAPITDFYFOO 154
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RESULT 15

IL1RA BOVIN STANDARD; PRT; 174 AA.
 ID IL1RA_BOVIN
 AC 077482;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (IRAP)
 DE (IL1 inhibitor) (IL-1RN).
 GN Name=IL1RN;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OX NCBI_Taxid=9913;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98305607; PubMed=9643454; DOI=10.1016/S0165-2427(98)00099-3;
 RA Kiriawa R., Fukuda T., Yamana H., Hagiwara K., Goto M., Obata Y.,
 RA Yoshino T., Iwai H.;
 RT "Enzymatic amplification and expression of bovine interleukin-1
 receptor antagonist cDNA."
 RL Vet. Immunol. Immunopathol. 62:197-208(1998).
 CC -1- FUNCTION: Inhibits the activity of IL-1 by binding to its
 CC receptor. Has no IL-1 like activity.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR EMBL; AB005148; BAA31854.1; -; mRNA.
 DR HSSP; P18510; IL1R.
 DR SMR; 077482; 32-174.
 DR InterPro; IPR000975; Interleukin_1.
 DR InterPro; IPR003297; Interleukin_IL1RA.
 DR PANTHER; PTHR10078:SF2; InterleukinIL1RA; 1.
 DR Pfam; PF00340; IL1; 1.
 DR PRINTS; PR00264; INTERLEUKIN1.
 DR PRINTS; PR01360; INTERLEUKIN1X.
 DR ProDom; PD002536; Interleukin_1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.
 KW Glycoprotein; Signal.
 FT SIGNAL 1 23 By similarity.
 FT CHAIN 24 174 Interleukin-1 receptor antagonist
 FT FT N-linked (GLNac. . .) (Potential).
 FT CARBOHYD 107 107
 FT DISULFID 89 139 By similarity.
 SO SEQUENCE 174 AA; 19926 MW; 1B56E7F224F851F CRC64;

Query Match 36.8%; Score 301.5; DB 1; Length 174;
 Best Local Similarity 48.0%; Pred. No. 5.8e-23;
 Matches 71; Conservative 15; Mismatches 49; Indels 13; Gaps 4;

QY 10 FMKDSALIKVLYLHNNQLAGLHAEKVIKGEISVFNRLADSLSP-VILGVGGSGQ 67
 Db 36 FRIMVNOGKIFILRNQLVAGVLOGPNTQLBEKIDVP-----IEPTMELGHHGX 88
 QY 68 CLSCGTEKGPILKLEPVNIMELYLAKESKSPFFYRRDMGLTSSPESAAYPGPFCTSP 126
 Db 89 CLACVSGDEIKLKEAVNITDLNQRQDKKFAFIRFNGPTTSPESAACPGMFLCTSL 148
 QY 127 EADQPVRLTQIPEDPAMDAPITDFYFOO 154
 Db 149 EADQPVGLTMTPEA--LKVTKFFYFOO 173

Search completed: April 5, 2006, 15:12:39
 Job time : 231 secs

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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:06:37 ; Search time 26 Seconds
(without alignments)
496.054 Million cell updates/sec

Title: US-09-770-528-2
819

Perfect score: 1 MMVLSGALCFRMDKSAKVL.....IPEDPAMDAPITDFFQOCD 156
Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

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3: /cgn2_6/ptodata/1/aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/aa/PTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 819 | 100.0 | 156 | 2 | US-09-398-412B-13 |
| 2 | 809 | 98.8 | 154 | 2 | US-09-775-046-11 |
| 3 | 734 | 89.6 | 155 | 2 | US-09-417-455-5 |
| 4 | 734 | 89.6 | 155 | 2 | US-09-348-942-5 |
| 5 | 734 | 89.6 | 155 | 2 | US-09-316-081-5 |
| 6 | 734 | 89.6 | 155 | 2 | US-09-578-458-5 |
| 7 | 734 | 89.6 | 155 | 2 | US-09-522-964A-5 |
| 8 | 734 | 89.6 | 155 | 2 | US-09-457-626-5 |
| 9 | 734 | 89.6 | 155 | 2 | US-09-576-008-5 |
| 10 | 734 | 89.6 | 155 | 2 | US-09-949-016-6827 |
| 11 | 734 | 89.6 | 155 | 2 | US-09-775-046-2 |
| 12 | 734 | 89.6 | 187 | 2 | US-09-949-016-9356 |
| 13 | 393 | 48.0 | 80 | 2 | US-09-417-455-3 |
| 14 | 393 | 48.0 | 80 | 2 | US-09-348-942-3 |
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| 24 | 309 | 37.7 | 152 | 2 | US-09-316-081-2 |
| 25 | 309 | 37.7 | 152 | 2 | US-09-578-458-2 |
| 26 | 309 | 37.7 | 152 | 2 | US-09-522-964A-2 |
| 27 | 309 | 37.7 | 169 | 2 | US-09-316-081-4 |

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| 28 | 309 | 37.7 | 169 | 2 | US-09-578-458-4 | Sequence 4, Appl1 |
| 29 | 309 | 37.7 | 169 | 2 | US-09-522-964A-4 | Sequence 4, Appl1 |
| 30 | 309 | 37.7 | 200 | 2 | US-09-578-458-13 | Sequence 13, Appl1 |
| 31 | 309 | 37.7 | 200 | 2 | US-09-522-964A-13 | Sequence 13, Appl1 |
| 32 | 307.5 | 37.5 | 147 | 2 | US-09-775-046-7 | Sequence 7, Appl1 |
| 33 | 307.5 | 37.5 | 153 | 2 | US-08-798-414-2 | Sequence 2, Appl1 |
| 34 | 307.5 | 37.5 | 153 | 2 | US-09-131-247-2 | Sequence 2, Appl1 |
| 35 | 307.5 | 37.5 | 153 | 2 | US-09-131-247-4 | Sequence 4, Appl1 |
| 36 | 307.5 | 37.5 | 153 | 2 | US-09-784-623-2 | Sequence 2, Appl1 |
| 37 | 307.5 | 37.5 | 153 | 2 | US-09-784-623-4 | Sequence 4, Appl1 |
| 38 | 307.5 | 37.5 | 156 | 1 | US-08-476-860-10 | Sequence 10, Appl1 |
| 39 | 307.5 | 37.5 | 156 | 1 | US-08-910-733-10 | Sequence 10, Appl1 |
| 40 | 307.5 | 37.5 | 156 | 1 | US-08-910-884-10 | Sequence 10, Appl1 |
| 41 | 307.5 | 37.5 | 159 | 1 | US-08-459-811-2 | Sequence 2, Appl1 |
| 42 | 307.5 | 37.5 | 159 | 1 | US-08-484-598-2 | Sequence 2, Appl1 |
| 43 | 307.5 | 37.5 | 159 | 1 | US-08-459-092-2 | Sequence 2, Appl1 |
| 44 | 307.5 | 37.5 | 159 | 1 | US-08-459-814-2 | Sequence 2, Appl1 |
| 45 | 307.5 | 37.5 | 159 | 1 | US-08-425-232-2 | Sequence 2, Appl1 |

ALIGNMENTS

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RESULT 1
US-09-398-412B-13
; Sequence 13, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related r
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398, 412B
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-398-412B-13

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Best Local Similarity 100.0%; Pred. No. 2.9e-96;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MMVLSGALCFRMDKSAKVLVYHNNQLLAGLHAERVYKGEISVVPNRALDASLSPVIL 60
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QY      121 FLCTSPDAPVRLTQIPEDPAMDAPITDFFQOCD 156
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RESULT 2
US-09-775-046-11
; Sequence 11, Application US/09775046
; Patent No. 6843987
; GENERAL INFORMATION:
; APPLICANT: Debete, Johannes Eduard Maria Antonius
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01073K
; CURRENT APPLICATION NUMBER: US/09/775, 046

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CURRENT FILING DATE: 2001-02-01
 PRIOR APPLICATION NUMBER: 60/179,638
 PRIOR FILING DATE: 2000-02-02
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: Patent version 3.1
 SEQ ID NO 11
 LENGTH: 154
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-775-046-11

Query Match 98.8%; Score 809; DB 2; Length 154;
 Best Local Similarity 100.0%; Pred. No. 5,3e-95;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSGALCFRMDKSAKLVYLNHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVILG 62
 DB 1 VLSGALCFRMDKSAKLVYLNHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVILG 60
 QY 63 VGGSSQCLSGCTGTEKPIKLEPVNIMELYGAKESKFTFYRRDMGLTSSPESAAYPGMF 122
 DB 61 VGGSSQCLSGCTGTEKPIKLEPVNIMELYGAKESKFTFYRRDMGLTSSPESAAYPGMF 120
 QY 123 CTSPEADQPVRLTQIPEDPAMDAPITDFYFOOCD 156
 DB 121 CTSPEADQPVRLTQIPEDPAMDAPITDFYFOOCD 154

RESULT 3
 US-09-417-455-5
 Sequence 5, Application US/09417455
 Patent No. 6294655
 GENERAL INFORMATION:
 APPLICANT: Ford, John
 APPLICANT: Pace, Ann
 TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
 FILE REFERENCE: 28110/36328
 CURRENT APPLICATION NUMBER: US/09/417,455
 CURRENT FILING DATE: 1999-10-13
 PRIOR APPLICATION NUMBER: US 09/348,942
 PRIOR FILING DATE: 1999-07-07
 PRIOR APPLICATION NUMBER: PCT/US99/04291
 PRIOR FILING DATE: 1999-04-05
 PRIOR APPLICATION NUMBER: US 09/287,210
 PRIOR FILING DATE: 1999-04-05
 PRIOR APPLICATION NUMBER: US 09/251,370
 PRIOR FILING DATE: 1999-02-17
 PRIOR APPLICATION NUMBER: US 09/229,591
 PRIOR FILING DATE: 1999-01-13
 PRIOR APPLICATION NUMBER: US 09/127,698
 PRIOR FILING DATE: 1998-07-31
 PRIOR APPLICATION NUMBER: US 09/099,818
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: US 09/082,364
 PRIOR FILING DATE: 1998-05-20
 PRIOR APPLICATION NUMBER: US 09/079,909
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: US 09/055,010
 PRIOR FILING DATE: 1998-04-03
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 5
 LENGTH: 155
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-417-455-5

Query Match 89.6%; Score 734; DB 2; Length 155;
 Best Local Similarity 91.0%; Pred. No. 2e-85;
 Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
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DB 1 VLSGALCFRMDKSAKLVYLNHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVILG 60
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 DB 61 VGGSSQCLSGCTGTEKPIKLEPVNIMELYGAKESKFTFYRRDMGLTSSPESAAYPGMF 120
 QY 122 CTSPEADQPVRLTQIPEDPAMDAPITDFYFOOCD 156
 DB 121 CTSPEADQPVRLTQIPEDPAMDAPITDFYFOOCD 155

RESULT 4
 US-09-348-942-5
 Sequence 5, Application US/09348942
 Patent No. 6337072
 GENERAL INFORMATION:
 APPLICANT: John Ford
 APPLICANT: Pace, Ann
 TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
 FILE REFERENCE: 28110/35801
 CURRENT APPLICATION NUMBER: US/09/348,942
 CURRENT FILING DATE: 1999-07-07
 PRIOR APPLICATION NUMBER: PCT/US99/04291
 PRIOR FILING DATE: 1999-04-05
 PRIOR APPLICATION NUMBER: US 09/287,210
 PRIOR FILING DATE: 1999-04-05
 PRIOR APPLICATION NUMBER: US 09/251,370
 PRIOR FILING DATE: 1999-02-17
 PRIOR APPLICATION NUMBER: US 09/229,591
 PRIOR FILING DATE: 1999-01-13
 PRIOR APPLICATION NUMBER: US 09/127,698
 PRIOR FILING DATE: 1998-07-31
 PRIOR APPLICATION NUMBER: US 09/099,818
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: US 09/082,364
 PRIOR FILING DATE: 1998-05-20
 PRIOR APPLICATION NUMBER: US 09/079,909
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: US 09/055,010
 PRIOR FILING DATE: 1998-04-03
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 5
 LENGTH: 155
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-348-942-5

Query Match 89.6%; Score 734; DB 2; Length 155;
 Best Local Similarity 91.0%; Pred. No. 2e-85;
 Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
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 DB 1 VLSGALCFRMDKSAKLVYLNHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVILG 60
 QY 62 VGGSSQCLSGCTGTEKPIKLEPVNIMELYGAKESKFTFYRRDMGLTSSPESAAYPGMF 121
 DB 61 VGGSSQCLSGCTGTEKPIKLEPVNIMELYGAKESKFTFYRRDMGLTSSPESAAYPGMF 120
 QY 122 CTSPEADQPVRLTQIPEDPAMDAPITDFYFOOCD 156
 DB 121 CTSPEADQPVRLTQIPEDPAMDAPITDFYFOOCD 155

RESULT 5
 US-09-316-081-5
 Sequence 5, Application US/09316081
 Patent No. 6339141
 GENERAL INFORMATION:
 APPLICANT: Ballinger, Dennis G.
 APPLICANT: Pace, Ann M.
 TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
 FILE REFERENCE: 28110/35659

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; CURRENT APPLICATION NUMBER: US/09/316,081
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-316-081-5
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Query Match      89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
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      61 VQGSQCISCVGQEPITLLEPVNIMELYLGAKESKSTFFYRRDMGLTSSFESAAYPGWF 120
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RESULT 6
US-09-578-458-5
; Sequence 5, Application US/09578458
; Patent No. 6365726
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; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Ford, John
; APPLICANT: Ho, Alice
; APPLICANT: Lin, Hai Shan
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/36479
; CURRENT APPLICATION NUMBER: US/09/578,458
; CURRENT FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/522,964
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/316,086
; PRIOR FILING DATE: 1999-03-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-578-458-5
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Query Match      89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
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QY      2 MVLGALCFRMDKSLAKVLYHNNQLLAGLHAERKVGEEISVVPNRALDASISPVILG 61
      1 MVLGALCFRMDKSLAKVLYHNNQLLAGLHAERKVGEEISVVPNRALDASISPVILG 60
DB      62 VQGSQCISCCTEKGPILKLEPVNIMELYLGAKESKSTFFYRRDMGLTSSFESAAYPGWF 121
      61 VQGSQCISCVGQEPITLLEPVNIMELYLGAKESKSTFFYRRDMGLTSSFESAAYPGWF 120
QY      122 LCTSPADQPVRLTQIPEDPAMDAPITDFFYFOQCD 156
      121 LCTVPEADQPVRLTQLPENGGMNAPITDFFYFOQCD 155
DB
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RESULT 7
US-09-522-964A-5
; Sequence 5, Application US/09522964A
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; Patent No. 6372892
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Lin, Hai Shan
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/36210
; CURRENT APPLICATION NUMBER: US/09/522,964A
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/316,086
; PRIOR FILING DATE: 1999-03-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-522-964A-5
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Query Match      89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
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QY      2 MVLGALCFRMDKSLAKVLYHNNQLLAGLHAERKVGEEISVVPNRALDASISPVILG 61
      1 MVLGALCFRMDKSLAKVLYHNNQLLAGLHAERKVGEEISVVPNRALDASISPVILG 60
DB      62 VQGSQCISCCTEKGPILKLEPVNIMELYLGAKESKSTFFYRRDMGLTSSFESAAYPGWF 121
      61 VQGSQCISCVGQEPITLLEPVNIMELYLGAKESKSTFFYRRDMGLTSSFESAAYPGWF 120
QY      122 LCTSPADQPVRLTQIPEDPAMDAPITDFFYFOQCD 156
      121 LCTVPEADQPVRLTQLPENGGMNAPITDFFYFOQCD 155
DB
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RESULT 8
US-09-457-626-5
; Sequence 5, Application US/09457626
; Patent No. 6426191
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; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36010
; CURRENT APPLICATION NUMBER: US/09/457,626
; CURRENT FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 09/417,455
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 155
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-457-626-5

Query Match      89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 2 MVLGALCFRMDKSLKLYLHNNQLLAGLHAEKVIKGEISVVPNRALDASLSPVILG 61
DB 1 MVLGALCFRMDKSLKLYLHNNQLLAGLHAEKVIKGEISVVPNRALDASLSPVILG 60

OY 62 VGGSGCSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMDGLTSSPESAAYPGMF 121
DB 61 VGGSGCSCGCGVGEPTLTLEPVNIMELYLGAKESKSFYFRDMDGLTSSPESAAYPGMF 120

OY 122 LCTSPADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 LCTVPEADQPVRLTQIPEDPAMDAPITDFYFOQCD 155

RESULT 9
US-09-576-008-5
Sequence 5, Application US/09576008
Patent No. 6541623
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Ho, Alice Suk-Yue
TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
FILE REFERENCE: 28110/36456
CURRENT FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 09/523,552
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: US 09/457,626
PRIOR FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 09/417,455
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US 09/348,942
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: PCT/US99/04291
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: US 09/287,210
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: US 09/251,370
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: US 09/229,591
PRIOR FILING DATE: 1999-01-13
PRIOR APPLICATION NUMBER: US 09/127,698
PRIOR FILING DATE: 1998-07-31
PRIOR APPLICATION NUMBER: US 09/099,818
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: US 09/082,364
PRIOR FILING DATE: 1998-05-20
PRIOR APPLICATION NUMBER: US 09/079,909
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 09/055,010
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 155
TYPE: PRT
ORGANISM: Homo sapiens
US-09-576-008-5

Query Match      89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 2 MVLGALCFRMDKSLKLYLHNNQLLAGLHAEKVIKGEISVVPNRALDASLSPVILG 61
DB 1 MVLGALCFRMDKSLKLYLHNNQLLAGLHAEKVIKGEISVVPNRALDASLSPVILG 60
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DB 1 MVLGALCFRMDKSLKLYLHNNQLLAGLHAEKVIKGEISVVPNRALDASLSPVILG 60
OY 62 VGGSGCSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMDGLTSSPESAAYPGMF 121
DB 61 VGGSGCSCGCGVGEPTLTLEPVNIMELYLGAKESKSFYFRDMDGLTSSPESAAYPGMF 120

OY 122 LCTSPADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 LCTVPEADQPVRLTQIPEDPAMDAPITDFYFOQCD 155

RESULT 10
US-09-949-016-6827
Sequence 6827, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6827
LENGTH: 155
TYPE: PRT
ORGANISM: Human
US-09-949-016-6827

Query Match      89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 2 MVLGALCFRMDKSLKLYLHNNQLLAGLHAEKVIKGEISVVPNRALDASLSPVILG 61
DB 1 MVLGALCFRMDKSLKLYLHNNQLLAGLHAEKVIKGEISVVPNRALDASLSPVILG 60

OY 62 VGGSGCSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMDGLTSSPESAAYPGMF 121
DB 61 VGGSGCSCGCGVGEPTLTLEPVNIMELYLGAKESKSFYFRDMDGLTSSPESAAYPGMF 120

OY 122 LCTSPADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 LCTVPEADQPVRLTQIPEDPAMDAPITDFYFOQCD 155

RESULT 11
US-09-775-046-2
Sequence 2, Application US/09775046
Patent No. 6843987
GENERAL INFORMATION:
APPLICANT: Debets, Johannes Eduard Maria Antonius
APPLICANT: Timans, Jacqueline C.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: MAMMALIAN CYTOKINES, RECEPTORS, RELATED REAGENTS AND METHODS
FILE REFERENCE: DX01073K
CURRENT FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/179,638
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 155
TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-775-046-2
Query Match      89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY      2  MVLGALCFRMDKSLKLYLHNNQLAGLHAERVIKGEISVVPNRALDASLSPVILG 61
DB      1  MVLGALCFRMDKSLKLYLHNNQLAGLHAERVIKGEISVVPNRALDASLSPVILG 60

QY      62  VGGSGQCLSCGVEGEPFLTLLEPVNIMELYLGAKEKSKFTFYRDMGLTSSFESAAYPGWF 121
DB      61  VGGSGQCLSCGVEGEPFLTLLEPVNIMELYLGAKEKSKFTFYRDMGLTSSFESAAYPGWF 120

QY      122  LCTSPADQPVRLTQIPEDPAMDAPITDFFYFOQCD 156
DB      121  LCTVPADQPVRLTQLPENGMNAPITDFFYFOQCD 155

RESULT 12
US-09-949-016-9356
; Sequence 9356, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9356
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9356

Query Match      89.6%; Score 734; DB 2; Length 187;
Best Local Similarity 91.0%; Pred. No. 2.7e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY      2  MVLGALCFRMDKSLKLYLHNNQLAGLHAERVIKGEISVVPNRALDASLSPVILG 61
DB      3  MVLGALCFRMDKSLKLYLHNNQLAGLHAERVIKGEISVVPNRALDASLSPVILG 92

QY      62  VGGSGQCLSCGVEGEPFLTLLEPVNIMELYLGAKEKSKFTFYRDMGLTSSFESAAYPGWF 121
DB      93  VGGSGQCLSCGVEGEPFLTLLEPVNIMELYLGAKEKSKFTFYRDMGLTSSFESAAYPGWF 152

QY      122  LCTSPADQPVRLTQIPEDPAMDAPITDFFYFOQCD 156
DB      153  LCTVPADQPVRLTQLPENGMNAPITDFFYFOQCD 187

RESULT 13
US-09-417-455-3
; Sequence 3, Application US/09417455
; Patent No. 6294655
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36328
; CURRENT APPLICATION NUMBER: US/09/417,455
; CURRENT FILING DATE: 1999-10-13
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; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-417-455-3

Query Match      48.0%; Score 393; DB 2; Length 80;
Best Local Similarity 90.0%; Pred. No. 2.7e-42;
Matches 72; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      77  PHLKPEPVNIMELYLGAKEKSKFTFYRDMGLTSSFESAAYPGWFPLCTSPADQPVRLTQ 136
DB      1  PHLKPEPVNIMELYLGAKEKSKFTFYRDMGLTSSFESAAYPGWFPLCTSPADQPVRLTQ 60

QY      137  IPEDPAMDAPITDFFYFOQCD 156
DB      61  LPENGMNAPITDFFYFOQCD 80

RESULT 14
US-09-348-942-3
; Sequence 3, Application US/09348942
; Patent No. 6337072
; GENERAL INFORMATION:
; APPLICANT: John Ford
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/35801
; CURRENT APPLICATION NUMBER: US/09/348,942
; CURRENT FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 80
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-348-942-3

Query Match 48.0%; Score 393; DB 2; Length 80;
Best Local Similarity 90.0%; Pred. No. 2.7e-42;
Matches 72; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 77 PTLKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAYPGWFLCTSPADQPVRLTQ 136
DB 1 PTLLEPVNIMELYGAKESKSFYRRDMGLTSSFESAYPGWFLCTVPEADQPVRLTQ 60
QY 137 IPEDPAMDAPITDFFYQOCD 156
DB 61 LPENGWNAPIITDFFYQOCD 80

RESULT 15
US-09-457-626-3
Sequence 3, Application US/09457626
Patent No. 6426191
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Pace, Ann
TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
FILE REFERENCE: 28110/36010
CURRENT APPLICATION NUMBER: US/09/457,626
CURRENT FILING DATE: 1999-12-08
EARLIER APPLICATION NUMBER: US 09/417,455
EARLIER FILING DATE: 1999-10-13
EARLIER APPLICATION NUMBER: US 09/348,942
EARLIER FILING DATE: 1999-07-07
EARLIER APPLICATION NUMBER: PCT/US99/04291
EARLIER FILING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 09/287,210
EARLIER FILING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 09/251,370
EARLIER FILING DATE: 1999-02-17
EARLIER APPLICATION NUMBER: US 09/229,591
EARLIER FILING DATE: 1999-01-13
EARLIER APPLICATION NUMBER: US 09/127,698
EARLIER FILING DATE: 1998-07-31
EARLIER APPLICATION NUMBER: US 09/099,818
EARLIER FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: US 09/082,364
EARLIER FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: US 09/079,909
EARLIER FILING DATE: 1998-05-15
EARLIER APPLICATION NUMBER: US 09/055,010
EARLIER FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 80
TYPE: PRT
ORGANISM: Homo sapiens
US-09-457-626-3

Query Match 48.0%; Score 393; DB 2; Length 80;
Best Local Similarity 90.0%; Pred. No. 2.7e-42;
Matches 72; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 77 PTLKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAYPGWFLCTSPADQPVRLTQ 136
DB 1 PTLLEPVNIMELYGAKESKSFYRRDMGLTSSFESAYPGWFLCTVPEADQPVRLTQ 60
QY 137 IPEDPAMDAPITDFFYQOCD 156
DB 61 LPENGWNAPIITDFFYQOCD 80

Search completed: April 5, 2006, 15:07:11
Job time : 26 secs

Thu Apr 6 16:26:16 2006

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:07:22 ; Search time 45 Seconds
(without alignments)
1448.475 Million cell updates/sec

Title: US-09-770-528-2
Perfect score: 819
Sequence: 1 NMVLGALCFRMKDSALKVL.....IPEDPAWDAPITDFYQGD 156

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------------|--------------------|
| 1 | 819 | 100.0 | 156 | US-09-770-528-2 | Sequence 2, Appli |
| 2 | 819 | 100.0 | 156 | US-09-965-640-2 | Sequence 2, Appli |
| 3 | 819 | 100.0 | 156 | US-10-267-791-2 | Sequence 2, Appli |
| 4 | 819 | 100.0 | 156 | US-10-042-865-124 | Sequence 124, App |
| 5 | 819 | 100.0 | 156 | US-10-695-195-13 | Sequence 13, Appli |
| 6 | 819 | 100.0 | 156 | US-10-734-985-2 | Sequence 13, Appli |
| 7 | 819 | 100.0 | 156 | US-10-948-920-2 | Sequence 2, Appli |
| 8 | 819 | 100.0 | 156 | US-10-042-865-123 | Sequence 123, App |
| 9 | 814 | 99.4 | 155 | US-09-775-046-2 | Sequence 2, Appli |
| 10 | 809 | 98.8 | 154 | US-10-006-867-152 | Sequence 152, App |
| 11 | 768 | 93.8 | 146 | US-09-730-617-55 | Sequence 55, Appli |
| 12 | 734 | 89.6 | 155 | US-09-730-617-61 | Sequence 61, Appli |
| 13 | 734 | 89.6 | 155 | US-09-730-617-80 | Sequence 80, Appli |
| 14 | 734 | 89.6 | 155 | US-09-730-617-96 | Sequence 96, Appli |
| 15 | 734 | 89.6 | 155 | US-09-775-046-2 | Sequence 2, Appli |
| 16 | 734 | 89.6 | 155 | US-09-965-640-4 | Sequence 4, Appli |
| 17 | 734 | 89.6 | 155 | US-10-006-867-152 | Sequence 152, App |
| 18 | 734 | 89.6 | 155 | US-10-003-671A-5 | Sequence 5, Appli |
| 19 | 734 | 89.6 | 155 | US-10-063-547-152 | Sequence 152, App |
| 20 | 734 | 89.6 | 155 | US-10-063-551-152 | Sequence 152, App |
| 21 | 734 | 89.6 | 155 | US-10-139-833-10 | Sequence 10, Appli |
| 22 | 734 | 89.6 | 155 | US-10-063-616-152 | Sequence 152, App |
| 23 | 734 | 89.6 | 155 | US-10-063-569-152 | Sequence 152, App |
| 24 | 734 | 89.6 | 155 | US-10-063-513-152 | Sequence 152, App |
| 25 | 734 | 89.6 | 155 | US-10-063-515-152 | Sequence 152, App |
| 26 | 734 | 89.6 | 155 | US-10-063-512-152 | Sequence 152, App |
| 27 | 734 | 89.6 | 155 | US-10-063-502-152 | Sequence 152, App |

ALIGNMENTS

| | | | | | | |
|----|-----|------|-----|---|-------------------|-------------------|
| 28 | 734 | 89.6 | 155 | 4 | US-10-063-549-152 | Sequence 152, App |
| 29 | 734 | 89.6 | 155 | 4 | US-10-063-554-152 | Sequence 152, App |
| 30 | 734 | 89.6 | 155 | 4 | US-10-063-553-152 | Sequence 152, App |
| 31 | 734 | 89.6 | 155 | 4 | US-10-063-518-152 | Sequence 152, App |
| 32 | 734 | 89.6 | 155 | 4 | US-10-063-598-152 | Sequence 152, App |
| 33 | 734 | 89.6 | 155 | 4 | US-10-227-693-152 | Sequence 152, App |
| 34 | 734 | 89.6 | 155 | 4 | US-10-267-791-5 | Sequence 5, Appli |
| 35 | 734 | 89.6 | 155 | 4 | US-10-063-563-152 | Sequence 152, App |
| 36 | 734 | 89.6 | 155 | 4 | US-10-063-555-152 | Sequence 152, App |
| 37 | 734 | 89.6 | 155 | 4 | US-10-063-557-152 | Sequence 152, App |
| 38 | 734 | 89.6 | 155 | 4 | US-10-063-567-152 | Sequence 152, App |
| 39 | 734 | 89.6 | 155 | 4 | US-10-063-538-152 | Sequence 152, App |
| 40 | 734 | 89.6 | 155 | 4 | US-10-063-559-152 | Sequence 152, App |
| 41 | 734 | 89.6 | 155 | 4 | US-10-063-595-152 | Sequence 152, App |
| 42 | 734 | 89.6 | 155 | 4 | US-10-205-821-3 | Sequence 3, Appli |
| 43 | 734 | 89.6 | 155 | 4 | US-10-223-085-316 | Sequence 316, App |
| 44 | 734 | 89.6 | 155 | 4 | US-10-223-084-316 | Sequence 316, App |
| 45 | 734 | 89.6 | 155 | 4 | US-10-223-088-316 | Sequence 316, App |

RESULT 1
US-09-770-528-2
Sequence 2, Application US/09770528
Patent No. US20020164332A1
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
Sana, Theodore R.
Bazan, Fernando J.
Kastelein, Robert A.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,528
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/130,972
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/055,111
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: US 09/062,866
FILING DATE: 20-APR-1998
APPLICATION NUMBER: US 09/097,976
FILING DATE: 16-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0725K2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2;
US-09-770-528-2

Query Match 100.0%; Score 819; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.2e-84;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASLSPVIL 60
DB 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASLSPVIL 60

QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120

QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOCCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOCCD 156

RESULT 2
US-09-965-640-2

Sequence 2, Application US/09965640
Publication No. US20020187122A1

GENERAL INFORMATION:

APPLICANT: Sime, John E.

TITLE OF INVENTION: IL-1 DELTA DNA AND POLYPEPTIDES

FILE REFERENCE: 0315-C

CURRENT APPLICATION NUMBER: US/09/965,640

CURRENT FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: 09/612,921

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 156

TYPE: PRT

ORGANISM: Mus musculus

US-09-965-640-2

Query Match 100.0%; Score 819; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.2e-84;

Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASLSPVIL 60
DB 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASLSPVIL 60

QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120

QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOCCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOCCD 156

RESULT 3
US-10-267-791-2

Sequence 2, Application US/10267791

Publication No. US20030059892A1

GENERAL INFORMATION:

APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL MOLECULES OF THE TANGO-93-RELATED PROTEIN FAMILY

FILE REFERENCE: 07334-200001 (formerly 09404/086001)

CURRENT APPLICATION NUMBER: US/10/267,791

CURRENT FILING DATE: 2002-10-09

PRIOR APPLICATION NUMBER: US/09/369,693

PRIOR FILING DATE: 1999-08-06

PRIOR APPLICATION NUMBER: US 09/131,263

PRIOR FILING DATE: 1998-08-07

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 156

TYPE: PRT

ORGANISM: Mus musculus

US-10-267-791-2

Query Match 100.0%; Score 819; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.2e-84;

Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASLSPVIL 60
DB 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASLSPVIL 60

QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120

QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOCCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOCCD 156

RESULT 4
US-10-042-865-124

Sequence 124, Application US/10042865

Publication No. US20040029216A1

GENERAL INFORMATION:

APPLICANT: Padigaru, Muralidhara

APPLICANT: Li, Li

APPLICANT: Zernhusen, Bryan D

APPLICANT: Casman, Stacie J

APPLICANT: Shenoy, Suresh G

APPLICANT: Spytek, Kimberly

APPLICANT: Zhong, Mei

APPLICANT: Gangoli, Esba A

APPLICANT: Burgess, Catherine E

APPLICANT: Patuturajan, Meera

APPLICANT: Vernet, Corine A.M

APPLICANT: Taylor, Sarah

APPLICANT: Tchernev, Vellizar T

APPLICANT: Miller, Charles E

APPLICANT: Guo, Xiaojia

APPLICANT: Boldog, Ference L

APPLICANT: Grose, William M

APPLICANT: Alsobrook II, John P

APPLICANT: Gerlach, Valerie L

APPLICANT: Reisinger, Shlomit R

APPLICANT: Rothenberg, Mark E

APPLICANT: Ellerman, Karen

APPLICANT: MacDougall, John

APPLICANT: Malvankar, Uriel M

APPLICANT: Millet, Isabelle

APPLICANT: Peyman, John

APPLICANT: Smitson, Gienna

APPLICANT: Gunther, Erik

APPLICANT: Stone, David

TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of

FILE REFERENCE: 21402-537

CURRENT APPLICATION NUMBER: US/10/042,865

CURRENT FILING DATE: 2002-05-17

PRIOR APPLICATION NUMBER: 60/260,417

PRIOR FILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: 60/260,831

PRIOR FILING DATE: 2001-01-10

PRIOR APPLICATION NUMBER: 60/272,338

PRIOR FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: 60/274,876

PRIOR FILING DATE: 2001-03-09

PRIOR APPLICATION NUMBER: 60/284,704

PRIOR FILING DATE: 2001-04-18

NUMBER OF SEQ ID NOS: 264
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 124
LENGTH: 156
TYPE: PRT
ORGANISM: Mus musculus
US-10-042-865-124

Query Match 100.0%; Score 819; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2,2e-84;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRKMDSALKVLYLHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVIL 60
DB 1 MMVLSGALCFRKMDSALKVLYLHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 5

US-10-695-195-13
Sequence 13, Application US/10695195
Publication No. US20040068099A1

GENERAL INFORMATION:

APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: DMAX Research Institute
STREET: 901 California Avenue

CITY: Palo Alto
STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/695,195
FILING DATE: 27-Oct-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/398,412
FILING DATE: 17-Sep-1999

ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0904K

TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-695-195-13

Query Match 100.0%; Score 819; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2,2e-84;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRKMDSALKVLYLHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVIL 60
DB 1 MMVLSGALCFRKMDSALKVLYLHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 6

US-10-694-978-13
Sequence 13, Application US/10694978
Publication No. US20040087766A1

GENERAL INFORMATION:

APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: DMAX Research Institute
STREET: 901 California Avenue

CITY: Palo Alto
STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/694,978
FILING DATE: 27-Oct-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/398,412
FILING DATE: 17-Sep-1999

ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0904K

TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-694-978-13

Query Match 100.0%; Score 819; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2,2e-84;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRKMDSALKVLYLHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVIL 60
DB 1 MMVLSGALCFRKMDSALKVLYLHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 7

US-10-734-985-2
; Sequence 2, Application US/10734985
; Publication No. US20040142420A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TANGO-93-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-369001
; CURRENT APPLICATION NUMBER: US/10/734,985
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US/10/134,410
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 09/131,263
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: US 09/369,693
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-734-985-2

Query Match 100.0%; Score 819; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2,2e-84;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTLSGALCFRMDASLKVLVYLNHNNLLAGGLHAKEVYIKGEESVVPNRALDASLSFVIL 60
DB 1 MMTLSGALCFRMDASLKVLVYLNHNNLLAGGLHAKEVYIKGEESVVPNRALDASLSFVIL 60
QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120
DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOOCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOOCD 156
RESULT 8
US-10-948-920-2
; Sequence 2, Application US/10948920
; Publication No. US20050058625A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; TITLE OF INVENTION: IL-1 DELTA DNA AND POLYPEPTIDES
; FILE REFERENCE: 0315-C
; CURRENT APPLICATION NUMBER: US/10/948,920
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US/09/965,640
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/612,921
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-948-920-2

Query Match 100.0%; Score 819; DB 5; Length 156;
Best Local Similarity 100.0%; Pred. No. 2,2e-84;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTLSGALCFRMDASLKVLVYLNHNNLLAGGLHAKEVYIKGEESVVPNRALDASLSFVIL 60
DB 1 MMTLSGALCFRMDASLKVLVYLNHNNLLAGGLHAKEVYIKGEESVVPNRALDASLSFVIL 60

QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120
DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOOCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOOCD 156

RESULT 9

US-10-042-865-123
; Sequence 123, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zernusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangoli, Bsha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchertnev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Reference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-042-865-123

Query Match 99.4%; Score 814; DB 4; Length 155;
Best Local Similarity 100.0%; Pred. No. 8,1e-84;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MMTLSGALCFRMDASLKVLVYLNHNNLLAGGLHAKEVYIKGEESVVPNRALDASLSFVIL 61
DB 1 MMTLSGALCFRMDASLKVLVYLNHNNLLAGGLHAKEVYIKGEESVVPNRALDASLSFVIL 60

QY 62 VGGGSCCSCGTEKGPILKLEPNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 121
DB 61 VGGGSCCSCGTEKGPILKLEPNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 120
QY 122 LCTSPDADQVRLTQIPEDPAMDAPITDIFYPOCCD 156
DB 121 LCTSPDADQVRLTQIPEDPAMDAPITDIFYPOCCD 155

RESULT 10
US-09-775-046-11
; Sequence 11, Application US/09775046
; Patent No. US20020102234A1
; GENERAL INFORMATION:
; APPLICANT: Debets, Johannes Eduard Maria Antonius
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01073K
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/179,638
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-775-046-11

Query Match 98.8%; Score 809; DB 3; Length 154;
Best Local Similarity 100.0%; Pred. No. 3e-83;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 VLSGALCFRMDKSAKLYLHNNQLLAGLHAERKVIKGEISVVPNRALDASLSPVILGV 62
DB 1 VLSGALCFRMDKSAKLYLHNNQLLAGLHAERKVIKGEISVVPNRALDASLSPVILGV 60
QY 63 QGGSCCSCGTEKGPILKLEPNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 122
DB 61 QGGSCCSCGTEKGPILKLEPNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 120
QY 123 CTSPEADQVRLTQIPEDPAMDAPITDIFYPOCCD 156
DB 121 CTSPEADQVRLTQIPEDPAMDAPITDIFYPOCCD 154

RESULT 11
US-09-730-617-55
; Sequence 55, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shinkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zeehuizen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: No. US20020068279A1 Proteins and Nucleic Acids Encoding the Same
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730,617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10

; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-730-617-55

Query Match 93.8%; Score 768; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.2e-78;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 CFRMDKSAKLYLHNNQLLAGLHAERKVIKGEISVVPNRALDASLSPVILGVGGSCC 68
DB 1 CFRMDKSAKLYLHNNQLLAGLHAERKVIKGEISVVPNRALDASLSPVILGVGGSCC 60
QY 69 LSCGTEKGPILKLEPNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWFCTSPDA 128
DB 61 LSCGTEKGPILKLEPNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWFCTSPDA 120
QY 129 DQVRLTQIPEDPAMDAPITDIFYPOCCD 154
DB 121 DQVRLTQIPEDPAMDAPITDIFYPOCCD 146

RESULT 12
US-09-730-617-61
; Sequence 61, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shinkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zeehuizen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: No. US20020068279A1 Proteins and Nucleic Acids Encoding the Same
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730,617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-730-617-61

Query Match 89.6%; Score 734; DB 3; Length 155;
Best Local Similarity 91.0%; Pred. No. 9.6e-75;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 2 MVSGLACFRMDKSAKLYLHNNQLLAGLHAERKVIKGEISVVPNRALDASLSPVILGV 61
DB 1 MVSGLACFRMDKSAKLYLHNNQLLAGLHAERKVIKGEISVVPNRALDASLSPVILGV 60
QY 62 VGGGSCCSCGTEKGPILKLEPNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 121
DB 61 VGGGSCCSCGTEKGPILKLEPNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 120
QY 122 LCTSPDADQVRLTQIPEDPAMDAPITDIFYPOCCD 156

Thu Apr 6 16:26:16 2006

us-09-770-528-2.rapbm

Page 6

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

RESULT 13
US-09-730-617-80

Sequence 80, Application US/09730617
Patent No. US20020068279A1

GENERAL INFORMATION:

APPLICANT: Burgess, Catherine E

APPLICANT: Prayaga, Sudhirdas K

APPLICANT: Shinkets, Richard A

APPLICANT: Raestelli, Luca

APPLICANT: Zernhusen, Bryan D

APPLICANT: Mezes, Peter S

TITLE OF INVENTION: No. US20020068279A1el Proteins and Nucleic Acids Encoding the Sam

FILE REFERENCE: 15966-609 US/09/730,617

CURRENT FILING DATE: 2000-12-05

PRIOR APPLICATION NUMBER: 60/169,056

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 60/169,886

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 60/170,252

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: 60/175,740

PRIOR FILING DATE: 2000-01-12

NUMBER OF SEQ ID NOS: 100

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 80

LENGTH: 155

TYPE: PRT

ORGANISM: Homo sapiens

US-09-730-617-80

Query Match 89.6%; Score 734; DB 3; Length 155;
Best Local Similarity 91.0%; Pred. No. 9.6e-75;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 MVLGALCFPMKDSALKVLYLHNNQLLAGLHAEKVIKGEISVPPRRLDASISPVILG 61

Db 1 MVLGALCFPMKDSALKVLYLHNNQLLAGLHAEKVIKGEISVPPRRLDASISPVILG 60

QY 62 VQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWF 121

Db 61 VQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWF 120

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

RESULT 14

US-09-730-617-96

Sequence 96, Application US/09730617

Patent No. US20020068279A1

GENERAL INFORMATION:

APPLICANT: Burgess, Catherine E

APPLICANT: Prayaga, Sudhirdas K

APPLICANT: Shinkets, Richard A

APPLICANT: Raestelli, Luca

APPLICANT: Zernhusen, Bryan D

APPLICANT: Mezes, Peter S

TITLE OF INVENTION: No. US20020068279A1el Proteins and Nucleic Acids Encoding the Sam

FILE REFERENCE: 15966-609 US/09/730,617

CURRENT FILING DATE: 2000-12-05

PRIOR APPLICATION NUMBER: 60/169,056

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 60/169,886

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 60/169,886

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 60/170,252

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: 60/175,740

PRIOR FILING DATE: 2000-01-12

NUMBER OF SEQ ID NOS: 100

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 96

LENGTH: 155

TYPE: PRT

ORGANISM: Homo sapiens

US-09-730-617-96

Query Match 89.6%; Score 734; DB 3; Length 155;
Best Local Similarity 91.0%; Pred. No. 9.6e-75;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 MVLGALCFPMKDSALKVLYLHNNQLLAGLHAEKVIKGEISVPPRRLDASISPVILG 61

Db 1 MVLGALCFPMKDSALKVLYLHNNQLLAGLHAEKVIKGEISVPPRRLDASISPVILG 60

QY 62 VQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWF 121

Db 61 VQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWF 120

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

RESULT 15

US-09-775-046-2

Sequence 2, Application US/09775046

Patent No. US20020102234A1

GENERAL INFORMATION:

APPLICANT: Debets, Johannes Eduard Maria Antonius

APPLICANT: Timans, Jacqueline C.

APPLICANT: Bazan, J. Fernando

APPLICANT: Kastelein, Robert A.

TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS

FILE REFERENCE: DX01073K US/09/775,046

CURRENT APPLICATION NUMBER: 2001-02-01

PRIOR FILING DATE: 2000-02-02

PRIOR APPLICATION NUMBER: 60/179,638

PRIOR FILING DATE: 2000-02-02

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 155

TYPE: PRT

ORGANISM: Homo sapiens

US-09-775-046-2

Query Match 89.6%; Score 734; DB 3; Length 155;
Best Local Similarity 91.0%; Pred. No. 9.6e-75;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 MVLGALCFPMKDSALKVLYLHNNQLLAGLHAEKVIKGEISVPPRRLDASISPVILG 61

Db 1 MVLGALCFPMKDSALKVLYLHNNQLLAGLHAEKVIKGEISVPPRRLDASISPVILG 60

QY 62 VQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWF 121

Db 61 VQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWF 120

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

Search completed: April 5, 2006, 15:08:15
Job time : 46 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:08:22 ; Search time 14 Seconds
(without alignments)
347.568 Million cell updates/sec

Title: US-09-770-528-2

Perfect score: 819
Sequence: 1 MMTLSGALCFRMKDSALKVL.....IPEDPAMDAPITDPTFFOCCD 156

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDS5/ptodata/1/pubpaa/US08_NEM_PUB pep: *
2: /SIDS5/ptodata/1/pubpaa/US07_NEM_PUB pep: *
3: /SIDS5/ptodata/1/pubpaa/US07_NEM_PUB pep: *
4: /SIDS5/ptodata/1/pubpaa/PCF_NEM_PUB pep: *
5: /SIDS5/ptodata/1/pubpaa/US09_NEM_PUB pep: *
6: /SIDS5/ptodata/1/pubpaa/US10_NEM_PUB pep: *
7: /SIDS5/ptodata/1/pubpaa/US11_NEM_PUB pep: *
8: /SIDS5/ptodata/1/pubpaa/US60_NEM_PUB pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------------|--------------------|
| 1 | 734 | 89.6 | 155 | US-10-063-703-152 | Sequence 152, App |
| 2 | 734 | 89.6 | 155 | US-11-102-240-152 | Sequence 152, App |
| 3 | 734 | 89.6 | 155 | US-11-103-195-152 | Sequence 152, App |
| 4 | 307.5 | 37.5 | 143 | US-10-995-561-568 | Sequence 568, App |
| 5 | 307.5 | 37.5 | 143 | US-10-995-561-569 | Sequence 569, App |
| 6 | 307.5 | 37.5 | 143 | US-10-995-561-570 | Sequence 570, App |
| 7 | 307.5 | 37.5 | 152 | US-11-097-993-3 | Sequence 3, Appl |
| 8 | 307.5 | 37.5 | 152 | US-11-097-993-3 | Sequence 3, Appl |
| 9 | 307.5 | 37.5 | 153 | US-11-097-993-5 | Sequence 5, Appl |
| 10 | 307.5 | 37.5 | 153 | US-11-097-993-5 | Sequence 5, Appl |
| 11 | 307.5 | 37.5 | 153 | US-11-175-734-5 | Sequence 5, Appl |
| 12 | 307.5 | 37.5 | 159 | US-10-995-561-567 | Sequence 567, App |
| 13 | 307.5 | 37.5 | 159 | US-11-097-993-6 | Sequence 6, Appl |
| 14 | 307.5 | 37.5 | 159 | US-11-097-993-13 | Sequence 13, Appl |
| 15 | 307.5 | 37.5 | 177 | US-10-995-561-571 | Sequence 571, Appl |
| 16 | 307.5 | 37.5 | 177 | US-10-876-787-4 | Sequence 4, Appl |
| 17 | 307.5 | 37.5 | 177 | US-11-097-993-2 | Sequence 2, Appl |
| 18 | 307.5 | 37.5 | 177 | US-11-097-993-2 | Sequence 2, Appl |
| 19 | 306.5 | 37.4 | 153 | US-11-097-453-12 | Sequence 12, Appl |
| 20 | 191.5 | 23.4 | 193 | US-10-063-703-142 | Sequence 142, App |
| 21 | 191.5 | 23.4 | 193 | US-11-102-240-142 | Sequence 142, App |
| 22 | 191.5 | 23.4 | 193 | US-11-103-195-142 | Sequence 142, App |
| 23 | 191.5 | 23.4 | 193 | US-11-103-195-142 | Sequence 142, App |
| 24 | 122 | 14.9 | 269 | US-10-995-561-535 | Sequence 535, App |
| 25 | 113 | 13.8 | 33 | US-11-072-170A-16 | Sequence 16, Appl |

| | | | | | | |
|----|------|------|------|---|----------------------|-------------------|
| 26 | 84 | 10.3 | 1433 | 7 | US-11-094-519A-40 | Sequence 40, Appl |
| 27 | 81 | 9.9 | 715 | 7 | US-11-087-099-2922 | Sequence 2922, Ap |
| 28 | 72.5 | 8.9 | 237 | 7 | US-11-096-568A-21493 | Sequence 21493, A |
| 29 | 72.5 | 8.9 | 247 | 7 | US-11-096-568A-21492 | Sequence 21492, A |
| 30 | 72.5 | 8.9 | 256 | 7 | US-11-096-568A-21491 | Sequence 21491, A |
| 31 | 72 | 8.8 | 666 | 7 | US-11-096-568A-14747 | Sequence 14747, A |
| 32 | 72 | 8.8 | 761 | 7 | US-11-096-568A-14746 | Sequence 14746, A |
| 33 | 72 | 8.8 | 911 | 7 | US-11-096-568A-14745 | Sequence 14745, A |
| 34 | 71.5 | 8.7 | 1147 | 7 | US-11-087-099-11762 | Sequence 11762, A |
| 35 | 71.5 | 8.7 | 4060 | 6 | US-10-922-232B-55 | Sequence 55, Appl |
| 36 | 71.5 | 8.7 | 6738 | 7 | US-10-922-232B-55 | Sequence 56, Appl |
| 37 | 70.5 | 8.6 | 548 | 7 | US-11-096-568A-26923 | Sequence 26923, A |
| 38 | 70.5 | 8.6 | 663 | 7 | US-11-096-568A-26923 | Sequence 26923, A |
| 39 | 70.5 | 8.6 | 699 | 7 | US-11-096-568A-26922 | Sequence 26922, A |
| 40 | 70.5 | 8.6 | 841 | 6 | US-10-770-726-88 | Sequence 88, Appl |
| 41 | 70.5 | 8.6 | 857 | 7 | US-11-090-617-686 | Sequence 686, App |
| 42 | 69.5 | 8.5 | 29 | 7 | US-11-072-170A-17 | Sequence 17, Appl |
| 43 | 69.5 | 8.5 | 311 | 7 | US-11-096-568A-27013 | Sequence 27013, A |
| 44 | 69.5 | 8.5 | 340 | 7 | US-11-096-568A-27013 | Sequence 27013, A |
| 45 | 69.5 | 8.5 | 366 | 7 | US-11-096-568A-28853 | Sequence 28853, A |

ALIGNMENTS

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RESULT 1
US-10-063-703-152
; Sequence 152, Application US/10063703
; Publication No. US20060080901A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerltsoff, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,703
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 152
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-703-152

Query Match      89.6%; Score 734; DB 6; Length 155;
Best local Similarity 91.0%; Pred No. 1,1e-72;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY      2 MVLGALCFRMKDSALKVL...YLNNOQLAGLAHAEKVIKKEBSVVRNALDASLSPITLG 61
DB      1 MMTLSGALCFRMKDSALKVL...YLNNOQLAGLAHAEKVIKKEBSVVRNALDASLSPITLG 60

QY      62 VGGSGCSCSGGEGEPTLTLEFVNIMELYLAKESGSPFFRRDKLTSFESAAYPGWR 121
DB      61 VGGSGCSCSGGEGEPTLTLEFVNIMELYLAKESGSPFFRRDKLTSFESAAYPGWR 120

QY      122 LCTSPADQPVRLTQIIPEDPAMDAPITDPTFFOCCD 156
DB      121 LCTVPADQPVRLTQIIPEDPAMDAPITDPTFFOCCD 155

RESULT 2
US-11-102-240-152
; Sequence 152, Application US/11102240
; Publication No. US20050260647A1

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```
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS
TITLE OF INVENTION: ESOPHAGEAL TUMOR
FILE REFERENCE: P3230R1C106C
CURRENT APPLICATION NUMBER: US/11/102,240
CURRENT FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 10/063662
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 10/006867
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 199-12-09
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 152
LENGTH: 155
TYPE: PRT
ORGANISM: Homo Sapien
US-11-102-240-152

Query Match
Best Local Similarity 89.6%; Score 734; DB 7; Length 155;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 MVLGALCFRMDKSAIKVLYLHNNQLLAGLHAKEVYKKEEISVVENRALDASLPVILG 61
DB 1 MVLGALCFRMDKSAIKVLYLHNNQLLAGLHAKEVYKKEEISVVENRALDASLPVILG 60
QY 62 VOGSGQCLSCGTEKGPILKLEPNIMELYGAKESKSFYFRDMGLTSSFESAAYPGWF 121
DB 61 VOGSGQCLSCGTEKGPILKLEPNIMELYGAKESKSFYFRDMGLTSSFESAAYPGWF 120

QY 122 LCTSPDAPVRLTOIPEDPAMDPTIDPFYFOOCD 156
DB 121 LCTVPEADQPVRLTOIPEDPAMDPTIDPFYFOOCD 155

RESULT 3
US-11-103-195-152
Sequence 152, Application US/11103195
Publication No. US20060051779A1
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230C166C1
CURRENT APPLICATION NUMBER: US/11/103,195
CURRENT FILING DATE: 2005-04-11
PRIOR APPLICATION NUMBER: 10/063743
PRIOR FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: 10/006867
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 152
LENGTH: 155
TYPE: PRT
ORGANISM: Homo Sapien
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US-11-103-195-152

Query Match
Best Local Similarity 89.6%; Score 734; DB 7; Length 155;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 MVLGALCFRMDKSAIKVLYLHNNQLLAGLHAKEVYKKEEISVVENRALDASLPVILG 61
DB 1 MVLGALCFRMDKSAIKVLYLHNNQLLAGLHAKEVYKKEEISVVENRALDASLPVILG 60
QY 62 VOGSGQCLSCGTEKGPILKLEPNIMELYGAKESKSFYFRDMGLTSSFESAAYPGWF 121
DB 61 VOGSGQCLSCGTEKGPILKLEPNIMELYGAKESKSFYFRDMGLTSSFESAAYPGWF 120

QY 122 LCTSPDAPVRLTOIPEDPAMDPTIDPFYFOOCD 156
DB 121 LCTVPEADQPVRLTOIPEDPAMDPTIDPFYFOOCD 155

RESULT 4
US-10-995-561-568
Sequence 568, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: C1001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 568
LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-568

Query Match
Best Local Similarity 37.5%; Score 307.5; DB 6; Length 143;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY 10 FRMKDSALIKVLYLHNNQLLAGLHAKEVYKKEEISVVENRALDASLP--VILGVGSGQ 67
DB 4 FRIMDVNOKTFYLRNNQLVAGYLQGPVNLBEKIDVP-----IEPRALFLGIGHGK 56
QY 68 CLSC--GTEKGPILKLEPNIMELYGAKESKSFYFRDMGLTSSFESAAYPGWFILCT 124
DB 57 CLSCVKSDETR--IQLEAVNITDISENRKQKRFAPFIRSDGPTTSSFSAACPGWFLCT 114

QY 125 SPADQPVRLTOIPEDPAMDPTIDPFYFOO 154
DB 115 AMEADQPVSLTNMPD---GVMTKTFYFOE 141

RESULT 5
US-10-995-561-569
Sequence 569, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: C1001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 569
LENGTH: 143
TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-995-561-569

Query Match
Best Local Similarity 37.5%; Score 307.5; DB 6; Length 143;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY 10 FRMDSALKVLYLHNNQLAGLHAKEYIKGEISVVPNRALDASLSP--VILGVQGSQ 67
DB 4 FRIMDVNQKTFYLRNNQLVAGYLOGPNNLEKIDVP-----IEPHALFLGIHGKM 56

QY 68 CLSC---GTEKGPILKLEPNVIMELYGAKESKSTFYRRDMGLTSSFESAAYPGWFLCT 124
DB 57 CLSCVKSDETR--LQLEAVNITDLSNRKQDKRFAFRSDSGPTTSFESAACPGWFLCT 114

QY 125 SPBADOVRLTQIPEDPAMDAPITDPFYFOQ 154
DB 115 AMEADQPVSLTNMPDE---GVMVTKFYFOE 141

RESULT 6
US-10-995-561-570
; Sequence 570, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 570
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-570

Query Match
Best Local Similarity 37.5%; Score 307.5; DB 6; Length 143;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY 10 FRMDSALKVLYLHNNQLAGLHAKEYIKGEISVVPNRALDASLSP--VILGVQGSQ 67
DB 4 FRIMDVNQKTFYLRNNQLVAGYLOGPNNLEKIDVP-----IEPHALFLGIHGKM 56

QY 68 CLSC---GTEKGPILKLEPNVIMELYGAKESKSTFYRRDMGLTSSFESAAYPGWFLCT 124
DB 57 CLSCVKSDETR--LQLEAVNITDLSNRKQDKRFAFRSDSGPTTSFESAACPGWFLCT 114

QY 125 SPBADOVRLTQIPEDPAMDAPITDPFYFOQ 154
DB 115 AMEADQPVSLTNMPDE---GVMVTKFYFOE 141

RESULT 7
US-11-097-993-3
; Sequence 3, Application US/11097993
; Publication No. US20050271618A1
; GENERAL INFORMATION:
; APPLICANT: Kerdin, Bruce
; TITLE OF INVENTION: METHODS OF REDUCING AGGREGATION OF IL-1RA
; FILE REFERENCE: 06843, 0093-00000
; CURRENT APPLICATION NUMBER: US/11/097,993
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/558,879
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 60/559,161
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 60/601,216
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; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/601,229
; PRIOR FILING DATE: 2004-08-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-097-993-3

Query Match
Best Local Similarity 37.5%; Score 307.5; DB 7; Length 152;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY 10 FRMDSALKVLYLHNNQLAGLHAKEYIKGEISVVPNRALDASLSP--VILGVQGSQ 67
DB 13 FRIMDVNQKTFYLRNNQLVAGYLOGPNNLEKIDVP-----IEPHALFLGIHGKM 65

QY 68 CLSC---GTEKGPILKLEPNVIMELYGAKESKSTFYRRDMGLTSSFESAAYPGWFLCT 124
DB 66 CLSCVKSDETR--LQLEAVNITDLSNRKQDKRFAFRSDSGPTTSFESAACPGWFLCT 123

QY 125 SPBADOVRLTQIPEDPAMDAPITDPFYFOQ 154
DB 124 AMEADQPVSLTNMPDE---GVMVTKFYFOE 150

RESULT 8
US-11-097-453-3
; Sequence 3, Application US/11097453
; Publication No. US20050282752A1
; GENERAL INFORMATION:
; APPLICANT: Kerdin, Bruce
; TITLE OF INVENTION: IL-1RA VARIANTS
; FILE REFERENCE: 06843, 0092-00000
; CURRENT APPLICATION NUMBER: US/11/097,453
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/558,879
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 60/601,216
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/559,161
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-097-453-3

Query Match
Best Local Similarity 37.5%; Score 307.5; DB 7; Length 152;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY 10 FRMDSALKVLYLHNNQLAGLHAKEYIKGEISVVPNRALDASLSP--VILGVQGSQ 67
DB 13 FRIMDVNQKTFYLRNNQLVAGYLOGPNNLEKIDVP-----IEPHALFLGIHGKM 65

QY 68 CLSC---GTEKGPILKLEPNVIMELYGAKESKSTFYRRDMGLTSSFESAAYPGWFLCT 124
DB 66 CLSCVKSDETR--LQLEAVNITDLSNRKQDKRFAFRSDSGPTTSFESAACPGWFLCT 123

QY 125 SPBADOVRLTQIPEDPAMDAPITDPFYFOQ 154
DB 124 AMEADQPVSLTNMPDE---GVMVTKFYFOE 150

RESULT 9
```

US-11-097-993-5
Sequence 5, Application US/11097993
Publication No. US20050271618A1
GENERAL INFORMATION:
APPLICANT: Raibekas, Andrei
APPLICANT: Kerwin, Bruce
TITLE OF INVENTION: METHODS OF REDUCING AGGREGATION OF IL-1RA
FILE REFERENCE: 06843.0093-00000
CURRENT APPLICATION NUMBER: US/11/097,993
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: 60/558,879
PRIOR FILING DATE: 2004-04-02
PRIOR APPLICATION NUMBER: 60/559,161
PRIOR FILING DATE: 2004-04-02
PRIOR APPLICATION NUMBER: 60/601,216
PRIOR FILING DATE: 2004-08-12
PRIOR APPLICATION NUMBER: 60/601,229
PRIOR FILING DATE: 2004-08-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5
LENGTH: 153
TYPE: PRN
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: anakinra sequence
US-11-097-993-5

Query Match 37.5%; Score 307.5; DB 7; Length 153;
Best Local Similarity 48.0%; Pred. No. 3.4e-26;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY 10 FRKDSALKVLYLHNNQLLAGLHAKEVYKGEISVVPNRALDASLP--VILGVQGSQ 67
DB 14 FRIMDVNOKTFYLRNNQVAGYLQGPVNLBEKIDVP-----IEPHALFLGIHGGM 66
QY 68 CLSC---GTEKGPILKEPVNIMELYLGAKESKSFYFRDMGLTSSPESAAVPGWFLCT 124
DB 67 CLSCVKSGBETR--LQLEAVNITDLSNRKQDKRFARISDSGPTTSFBSAACPGWFLCT 124
QY 125 SPADQPVRLTQIPEDPAMADPTDVFYFQ 154
DB 125 AMEADQPVSLTNMPDE---GWNVTKFYFQ 151

RESULT 10

US-11-097-453-5
Sequence 5, Application US/11097453
Publication No. US20050282752A1
GENERAL INFORMATION:
APPLICANT: Raibekas, Andrei
APPLICANT: Kerwin, Bruce
TITLE OF INVENTION: IL-1RA VARIANTS
FILE REFERENCE: 06843.0092-00000
CURRENT APPLICATION NUMBER: US/11/097,453
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: 60/558,879
PRIOR FILING DATE: 2004-04-02
PRIOR APPLICATION NUMBER: 60/601,216
PRIOR FILING DATE: 2004-08-12
PRIOR APPLICATION NUMBER: 60/601,229
PRIOR FILING DATE: 2004-08-12
PRIOR APPLICATION NUMBER: 60/559,161
PRIOR FILING DATE: 2004-04-02
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5
LENGTH: 153
TYPE: PRN
ORGANISM: Homo sapiens
US-11-097-453-5

Query Match 37.5%; Score 307.5; DB 7; Length 153;

Best Local Similarity 46.0%; Pred. No. 3.4e-26;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY 10 FRKDSALKVLYLHNNQLLAGLHAKEVYKGEISVVPNRALDASLP--VILGVQGSQ 67
DB 14 FRIMDVNOKTFYLRNNQVAGYLQGPVNLBEKIDVP-----IEPHALFLGIHGGM 66
QY 68 CLSC---GTEKGPILKEPVNIMELYLGAKESKSFYFRDMGLTSSPESAAVPGWFLCT 124
DB 67 CLSCVKSGBETR--LQLEAVNITDLSNRKQDKRFARISDSGPTTSFBSAACPGWFLCT 124
QY 125 SPADQPVRLTQIPEDPAMADPTDVFYFQ 154
DB 125 AMEADQPVSLTNMPDE---GWNVTKFYFQ 151

RESULT 11

US-11-175-734-5
Sequence 5, Application US/11175734
Publication No. US2006009389A1
GENERAL INFORMATION:
APPLICANT: Moore, Emma E.
APPLICANT: Ellsworth, Jeff L.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING FGF18 AND
FILE REFERENCE: 04-07
CURRENT APPLICATION NUMBER: US/11/175,734
CURRENT FILING DATE: 2005-07-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 153
TYPE: PRN
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: VARIANT
LOCATION: 1
OTHER INFORMATION: Xaa is Met or absent.
US-11-175-734-5

Query Match 37.5%; Score 307.5; DB 7; Length 153;
Best Local Similarity 48.0%; Pred. No. 3.4e-26;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY 10 FRKDSALKVLYLHNNQLLAGLHAKEVYKGEISVVPNRALDASLP--VILGVQGSQ 67
DB 14 FRIMDVNOKTFYLRNNQVAGYLQGPVNLBEKIDVP-----IEPHALFLGIHGGM 66
QY 68 CLSC---GTEKGPILKEPVNIMELYLGAKESKSFYFRDMGLTSSPESAAVPGWFLCT 124
DB 67 CLSCVKSGBETR--LQLEAVNITDLSNRKQDKRFARISDSGPTTSFBSAACPGWFLCT 124
QY 125 SPADQPVRLTQIPEDPAMADPTDVFYFQ 154
DB 125 AMEADQPVSLTNMPDE---GWNVTKFYFQ 151

RESULT 12

US-10-995-561-567
Sequence 567, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 567
LENGTH: 159

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-567

Query Match
Best Local Similarity 37.5%; Score 307.5; DB 6; Length 159;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY 10 FRMDSALKVLYLHNNOLLAGLHAEKYIKGEISVVPNRALDASLP--VILGVQGSQ 67
DB 20 FRIMDVNQKTFYLRNNQVAGYLQGPVNLBEKIDVP-----IEPHALFLGIHGKM 72
QY 68 CLSC---GTEKGPILKLEPVNIMELYGAKESKSFYFRDMLTSSFESAAYPGMFLCT 124
DB 73 CLSCVKSGBETR--LQLEAVNITDLSNRKODKRFATIRSDSGPTTSFESAACPGMFLCT 130
QY 125 SPBADOVRLTQIPEDPAMDAPITDFFYFOQ 154
DB 131 AMEADQPVSLTNMPDE---GVMVTKFYFOE 157

RESULT 13
US-11-097-993-6
; Sequence 6, Application US/11097993
; Publication No. US20050271618A1
; GENERAL INFORMATION:
; APPLICANT: Raibekas, Andrei
; TITLE OF INVENTION: METHODS OF REDUCING AGGREGATION OF IL-1RA
; FILE REFERENCE: 06843.0093-00000
; CURRENT APPLICATION NUMBER: US/11/097, 993
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/558, 879
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 60/559, 161
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 60/601, 216
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/601, 229
; PRIOR FILING DATE: 2004-08-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: icIL-1ra sequence
US-11-097-993-6

Query Match
Best Local Similarity 37.5%; Score 307.5; DB 7; Length 159;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY 10 FRMDSALKVLYLHNNOLLAGLHAEKYIKGEISVVPNRALDASLP--VILGVQGSQ 67
DB 20 FRIMDVNQKTFYLRNNQVAGYLQGPVNLBEKIDVP-----IEPHALFLGIHGKM 72
QY 68 CLSC---GTEKGPILKLEPVNIMELYGAKESKSFYFRDMLTSSFESAAYPGMFLCT 124
DB 73 CLSCVKSGBETR--LQLEAVNITDLSNRKODKRFATIRSDSGPTTSFESAACPGMFLCT 130
QY 125 SPBADOVRLTQIPEDPAMDAPITDFFYFOQ 154
DB 131 AMEADQPVSLTNMPDE---GVMVTKFYFOE 157

RESULT 14
US-11-097-453-13
; Sequence 13, Application US/11097453
; Publication No. US20050282752A1
; GENERAL INFORMATION:
; APPLICANT: Raibekas, Andrei
```

```

; APPLICANT: Kerwin, Bruce
; TITLE OF INVENTION: IL-1RA VARIANTS
; FILE REFERENCE: 06843.0092-00000
; CURRENT APPLICATION NUMBER: US/11/097, 453
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/558, 879
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 60/601, 216
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/601, 229
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/559, 161
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-097-453-13

Query Match
Best Local Similarity 37.5%; Score 307.5; DB 7; Length 159;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY 10 FRMDSALKVLYLHNNOLLAGLHAEKYIKGEISVVPNRALDASLP--VILGVQGSQ 67
DB 20 FRIMDVNQKTFYLRNNQVAGYLQGPVNLBEKIDVP-----IEPHALFLGIHGKM 72
QY 68 CLSC---GTEKGPILKLEPVNIMELYGAKESKSFYFRDMLTSSFESAAYPGMFLCT 124
DB 73 CLSCVKSGBETR--LQLEAVNITDLSNRKODKRFATIRSDSGPTTSFESAACPGMFLCT 130
QY 125 SPBADOVRLTQIPEDPAMDAPITDFFYFOQ 154
DB 131 AMEADQPVSLTNMPDE---GVMVTKFYFOE 157

RESULT 15
US-10-995-561-571
; Sequence 571, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995, 561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 571
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-571

Query Match
Best Local Similarity 37.5%; Score 307.5; DB 6; Length 177;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY 10 FRMDSALKVLYLHNNOLLAGLHAEKYIKGEISVVPNRALDASLP--VILGVQGSQ 67
DB 38 FRIMDVNQKTFYLRNNQVAGYLQGPVNLBEKIDVP-----IEPHALFLGIHGKM 90
QY 68 CLSC---GTEKGPILKLEPVNIMELYGAKESKSFYFRDMLTSSFESAAYPGMFLCT 124
DB 91 CLSCVKSGBETR--LQLEAVNITDLSNRKODKRFATIRSDSGPTTSFESAACPGMFLCT 148
QY 125 SPBADOVRLTQIPEDPAMDAPITDFFYFOQ 154
DB 149 AMEADQPVSLTNMPDE---GVMVTKFYFOE 175
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Thu Apr 6 16:26:16 2006

us-09-770-528-2.rapbn

Page 6

Search completed: April 5, 2006, 15:08:44
Job time : 14 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:08:52 ; Search time 81 Seconds
(without alignments)
846.211 Million cell updates/sec

Title: US-09-770-528-2

Perfect score: 156
Sequence: 1 MNTVSGALCFPMKDSALKVL.....IPEDPAMDAPITDTPYFOCCD 156

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 8

Total number of hits satisfying chosen parameters: 596

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

_A_Geneseq_21: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *
9: Geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 2 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 3 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 4 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 5 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 6 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 7 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 8 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 9 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 10 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 11 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 12 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 13 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 14 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 15 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 16 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 17 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 18 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 19 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 20 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 21 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 22 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 23 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |
| 24 | 156 | 100.0 | 156 | 2 | AAW86284 Rodent in |

| | | | | | |
|----|----|------|-----|---|--------------------|
| 25 | 44 | 28.2 | 147 | 5 | ABP52030 NOVINTRA |
| 26 | 44 | 28.2 | 147 | 6 | ABP97771 Amino aci |
| 27 | 44 | 28.2 | 147 | 7 | ADCT1444 Human NOV |
| 28 | 44 | 28.2 | 147 | 8 | ADN33855 Human NOV |
| 29 | 44 | 28.2 | 154 | 4 | AAW86284 Rodent in |
| 30 | 44 | 28.2 | 155 | 2 | AAW86284 Rodent in |
| 31 | 44 | 28.2 | 155 | 3 | AAW86284 Rodent in |
| 32 | 44 | 28.2 | 155 | 3 | AAW86284 Rodent in |
| 33 | 44 | 28.2 | 155 | 3 | AAW86284 Rodent in |
| 34 | 44 | 28.2 | 155 | 3 | AAW86284 Rodent in |
| 35 | 44 | 28.2 | 155 | 3 | AAW86284 Rodent in |
| 36 | 44 | 28.2 | 155 | 3 | AAW86284 Rodent in |
| 37 | 44 | 28.2 | 155 | 3 | AAW86284 Rodent in |
| 38 | 44 | 28.2 | 155 | 3 | AAW86284 Rodent in |
| 39 | 44 | 28.2 | 155 | 3 | AAW86284 Rodent in |
| 40 | 44 | 28.2 | 155 | 3 | AAW86284 Rodent in |
| 41 | 44 | 28.2 | 155 | 3 | AAW86284 Rodent in |
| 42 | 44 | 28.2 | 155 | 3 | AAW86284 Rodent in |
| 43 | 44 | 28.2 | 155 | 3 | AAW86284 Rodent in |
| 44 | 44 | 28.2 | 155 | 3 | AAW86284 Rodent in |
| 45 | 44 | 28.2 | 155 | 3 | AAW86284 Rodent in |

ALIGNMENTS

| | | |
|----------|---|----------------------------|
| RESULT 1 | AAW86284 | standard; protein; 156 AA. |
| ID | AAW86284 | |
| AC | AAW86284 | |
| DT | 19-FEB-1999 | (first entry) |
| XX | | |
| DE | Rodent interleukin (IL)-1 delta polypeptide. | |
| XX | | |
| KW | Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine; | |
| KW | Inflammatory response; immune system; diagnosis; agonist; antagonist; | |
| XX | chemokine. | |
| OS | Mus sp. | |
| XX | | |
| PN | W09847921-A1. | |
| XX | | |
| PD | 29-OCT-1998. | |
| XX | | |
| PF | 17-APR-1998; | 98WO-US006879. |
| XX | | |
| PR | 21-APR-1997; | 97US-00837627. |
| PR | 06-AUG-1997; | 97US-0055111P. |
| PA | (SCHE) SCHERING CORP. | |
| PI | Hedrick JA, Sana TR, Bazan JF, Kastelein RA; | |
| XX | | |
| DR | WPI; 1998-60976/51. | |
| XX | | |
| PT | Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g. regulating | |
| PT | the immune system and inflammatory responses. | |
| XX | | |
| PS | Claim 1; Page 89-90; 11pp; English. | |
| XX | | |
| CC | This represents a rodent interleukin (IL)-1 delta polypeptide. The | |
| CC | invention relates to a recombinant polypeptide that specifically binds | |
| CC | polyclonal antibodies (Abs) generated against a 12 consecutive amino acid | |
| CC | segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these | |
| CC | IL polypeptides are used to regulate a cell involved in an inflammatory | |
| CC | response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are | |
| CC | used to produce Abs and antigen-Ab complexes. The polypeptides, Abs and | |
| CC | the corresponding nucleic acids regulate development and/or the immune | |
| CC | system, and can be used to diagnose and treat conditions associated with | |
| CC | abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1 | |

CC epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,
CC IL-1RA, IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1
CC epsilon polypeptides may be used as a soluble polypeptide or as a fusion
CC protein with another cytokine or chemokine

CC Sequence 156 AA;

Query Match 100.0%; Score 156; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.2e-159;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASISPVIL 60
DB 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASISPVIL 60
QY 61 GVGGSGQLSCGTEKGPILKLEPVNIMELYGAKESKSTFYRRDMGLTSSFESAAYPGW 120
DB 61 GVGGSGQLSCGTEKGPILKLEPVNIMELYGAKESKSTFYRRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 2

AA928407 standard; protein; 156 AA.

AA928407;

28-SEP-1999 (first entry)

Mouse interleukin 1 delta.

Interleukin 1 delta; IL-1 delta; glaucoma; ectodermal dysplasia;

insulin-dependent diabetes mellitus; wrinkly skin syndrome;

T-cell leukemia; lymphoma; tibial muscular dystrophy.

Mus musculus.

MO9935268-A1.

15-JUL-1999.

08-JAN-1999; 99MO-US000514.

09-JAN-1998; 98US-0071074P.

01-JUN-1998; 98US-0087393P.

(IMMV) IMMUNEX CORP.

Sims JE;

WPI; 1999-458310/38.

N-PSDB; AAX89431.

Murine and Human interleukin 1 delta DNA, polypeptides and its fragments,
PT useful as molecular weight markers.

Claim 1; Page 67; 72pp; English.

CC The present sequence represents mouse interleukin 1 delta (IL-1 delta).
CC IL-1 delta proteins are useful for the determination of the molecular
CC weight of a sample protein. The protein and its fragments are useful as
CC controls for peptide fragmentation. This is useful for determining the
CC isoelectric point of a sample protein. Antibodies generated against IL-1
CC delta and its fragmented peptides can be used to enhance the accuracy of
CC these molecular weight markers to determine the apparent molecular weight
CC and isoelectric point of a sample protein. IL-1 delta can be used to
CC screen for potential inhibitors of activity associated with IL-1 delta
CC counter-structure molecules. IL-1 delta can also be used as therapeutic
CC agents for the treatment of diseases mediated by IL-1 delta. IL-1 delta
CC may be used as a reagent in studying the interleukin 1 (IL-1) signalling

CC pathway, or as a reagent to block IL-1 signalling. The IL-1 delta coding
CC sequences can be used to identify human chromosome 2, and to identify
CC genes associated with certain diseases, especially with region 2q11-12,
CC including glaucoma, ectodermal dysplasia, insulin-dependent diabetes
CC mellitus, wrinkly skin syndrome, T-cell leukemia/ lymphoma and tibial
CC muscular dystrophy

CC Sequence 156 AA;

Query Match 100.0%; Score 156; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.2e-159;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASISPVIL 60
DB 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASISPVIL 60
QY 61 GVGGSGQLSCGTEKGPILKLEPVNIMELYGAKESKSTFYRRDMGLTSSFESAAYPGW 120
DB 61 GVGGSGQLSCGTEKGPILKLEPVNIMELYGAKESKSTFYRRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 3

AA92260 standard; protein; 156 AA.

AA92260;

10-AUG-2000 (first entry)

Murine IL-1 homologue, zllia3.

Generic; interleukin-1, IL-1; homologue; zllia3; anti-inflammatory;

antagonist; pro-inflammatory; agonist; immunomodulator; antiarthritic;

antirheumatic; osteopathic; antibacterial; cytostatic;

immunosuppressive; antidiabetic; nephrotropic; vasotropic;

vulnerary; 2q14.

Mus musculus.

WO200020595-A1.

13-APR-2000.

08-OCT-1999; 99MO-US023533.

08-OCT-1998; 98US-00169745.

(ZYMO) ZYMOGENETICS INC.

Sheppard PO, West RR, Clegg CH;

WPI; 2000-303780/26.

N-PSDB; AAA09198.

Proteins useful for treatment of inflammatory conditions such as
PT rheumatoid arthritis and psoriasis are agonists or antagonists forms of
PT new interleukin-1 homologue.

Example 7; Page 59-60; 64pp; English.

CC This shows an interleukin-1 (IL-1) homologue, designated zllia3. A 350 bp
CC probe generated from the DNA sequence by PCR using AAA09199-200 was used
CC to analyze human northern blots. It is believed that zllia3 acts through
CC IL-1 receptors. In general, zllia3 proteins having a Lys residue at
CC position 148 will have anti-inflammatory activity (e.g. AA92256), whilst
CC those having Asp (see AA92254) or Glu at this position will have pro-
CC inflammatory action. Zllia3 is used to modulate an immune response in an
CC animal (claimed). Antagonists zllia3 forms may be used to treat or

CC prevent chronic inflammatory diseases such as rheumatoid arthritis,
CC osteoarthritis and Lyme arthritis, psoriasis, to reduce tissue damage
CC after ischemia, to treat septic shock, graft-versus-host disease and
CC leukemia. The antagonists may also alleviate inflammatory bowel disease
CC including Crohn's disease and ulcerative colitis, insulin-dependent
CC diabetes mellitus, acute pancreatitis, glomerulonephritis and cerebral
CC ischemia. Agonist forms of zila3 may promote wound healing by IL-1
CC effects on growth factor secretion and cell proliferation. They may also
CC treat infections, especially gastrointestinal infections

CC Sequence 156 AA;

Query Match 100.0%; Score 156; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.2e-159; Mismatches 0; Indels 0; Gaps 0;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAKLVYLNHNOQLAGLHAERKVKGEISVVPNRALDASLPYL 60
DB 1 MMVLSGALCFRMDKSAKLVYLNHNOQLAGLHAERKVKGEISVVPNRALDASLPYL 60

QY 61 GVGGSGQLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSFESAAYPGW 120
DB 61 GVGGSGQLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSFESAAYPGW 120

QY 121 FLCTSPADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 FLCTSPADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 4
AA45061
ID AA45061 standard; protein; 156 AA.
AC AA45061;
XX
XX 31-MAY-2000 (first entry)
DT
DB Murine TANGO-93 protein.

XX TANGO-93; cytokine; mouse; secreted protein; IL-1 expression; cancer;
XX interleukin-1 receptor antagonist; IL-1ra; inflammation; antiasthmatic;
XX immunosuppressive; antirheumatic; antiarthritic; antipsoriatic; asthma;
XX antiinflammatory; antibacterial; antulcer; cytoskeletal; immunomodulator;
XX osteopathic; dermatological; antidiabetic; psoriasis; ulcerative colitis;
XX graft vs.-host disease; rheumatoid arthritis; inflammatory bowel disease;
XX septic shock; cachexia; Crohn's disease; chronic myelogenous leukaemia;
XX liver disease; diabetes; osteoarthritis; Hodgkin's disease; Lyme disease;
XX autoimmune disease; myasthenia gravis; pharmacogenomic; diagnosis;
XX systemic lupus erythematosus; forensic; transgenic animal.

XX Mus sp.
XX WO200008045-A2.
XX
XX 17-FEB-2000.

XX 06-AUG-1999; 99WO-US017886.
XX
XX 07-AUG-1998; 98US-00131263.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
XX Pan Y;
XX
XX WPI; 2000-205669/18.
XX
XX N-PSDB; AA250811.

XX Isolated nucleic acid sequences encoding TANGO-93 polypeptide useful for
XX treating a variety of cellular processes e.g. asthma, rheumatoid
XX arthritis, psoriasis and autoimmune diseases.
XX
XX Claim 9; Fig 1; il3p; English.

CC The present sequence is the murine TANGO-93, a secreted protein, that
CC belongs to the cytokine superfamily. It plays a role similar to secreted
CC interleukin-1 receptor antagonist (IL-1ra) and its expression is
CC developmentally regulated in liver, heart and bone marrow. TANGO-93
CC modulates immune mediated inflammation and IL-1 gene or protein
CC expression. TANGO-93 is useful as a modulating agent for regulating
CC cellular processes like asthma, graft vs.-host disease, rheumatoid
CC arthritis, psoriasis, inflammatory bowel disease, septic shock,
CC ulcerative colitis, Crohn's disease, chronic myelogenous leukaemia,
CC cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme disease,
CC cachexia, and autoimmune diseases e.g. myasthenia gravis, autoimmune
CC diabetes and systemic lupus erythematosus. Partial TANGO-93 sequences are
CC useful in forensic biology, for diagnostic and prognostic assays,
CC prophylactic and therapeutic treatment and pharmacogenomics. The DNA
CC sequences are useful as hybridisation probes and primers, for isolation
CC of TANGO-93 sequence and for the creation of transgenic animals

CC Sequence 156 AA;

Query Match 100.0%; Score 156; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.2e-159; Mismatches 0; Indels 0; Gaps 0;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAKLVYLNHNOQLAGLHAERKVKGEISVVPNRALDASLPYL 60
DB 1 MMVLSGALCFRMDKSAKLVYLNHNOQLAGLHAERKVKGEISVVPNRALDASLPYL 60

QY 61 GVGGSGQLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSFESAAYPGW 120
DB 61 GVGGSGQLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSFESAAYPGW 120

QY 121 FLCTSPADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 FLCTSPADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 5
AB062869
ID AB062869 standard; protein; 156 AA.
AC AB062869;
XX
XX 11-SEP-2003 (first entry)
DT
DB Mouse secreted protein TANGO-93.

XX Mouse; TANGO-93; secreted protein; antiasthmatic; immunosuppressive;
XX antirheumatic; antiarthritic; antiinflammatory; antipsoriatic;
XX cytoskeletal; hepatotropic; antidiabetic; dermatological; gene therapy;
XX cytokine superfamily; asthma; graft versus-host disease; cancer;
XX rheumatoid arthritis; psoriasis; inflammatory bowel disease;
XX septic shock; ulcerative colitis; Crohn's disease; liver disease;
XX chronic myelogenous leukaemia; Hodgkin's disease; Lyme's disease;
XX cachexia; autoimmune diabetes; systemic lupus erythematosus.

XX Mus musculus.
XX US2003059892-A1.
XX
XX 27-MAR-2003.

XX 09-OCT-2002; 2002US-00267791.
XX
XX 07-AUG-1998; 98US-00131263.
XX
XX 06-AUG-1999; 99US-00369693.

XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Pan Y;
XX
XX WPI; 2003-521914/49.
XX
XX N-PSDB; ACD26633, ACD26634.

PT New TANGO-93 nucleic acid molecules and polypeptides useful for treating
 PT asthma, graft versus-host disease, rheumatoid arthritis, psoriasis,
 PT inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's
 PT disease, cancer.

PS Claim 8; Fig 1; 43pp; English.

CC The invention describes an isolated nucleic acid molecule (I) designated
 CC as TANGO-93, a secreted protein predicted to be a member of the cytokine
 CC superfamily. The polynucleotides, polypeptides compounds and methods are
 CC useful for treating asthma, graft versus-host disease, rheumatoid
 CC arthritis, psoriasis, inflammatory bowel disease, septic shock,
 CC ulcerative colitis, Crohn's disease, chronic myelogenous leukaemia,
 CC cancer, liver disease, Hodgkin's disease, Lyme's disease, cachexia,
 CC autoimmune diabetes or systemic lupus erythematosus. This is the amino
 CC acid sequence of mouse TANGO-93

SQ Sequence 156 AA;

Query Match 100.0%; Score 156; DB 7; Length 156;
 Best Local Similarity 100.0%; Pred. No. 4.2e-159;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMVLSGALCFRMDKSLKVLVYHNNQLAGGLHAEKVIKGEISVVPNRALDASISPVYL 60
 DB 1 MMVLSGALCFRMDKSLKVLVYHNNQLAGGLHAEKVIKGEISVVPNRALDASISPVYL 60
 OY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120
 DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120
 OY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFYQCCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFYQCCD 156

RESULT 6
 ADJ88315
 ID ADJ88315 standard; protein; 156 AA.

AC ADJ88315;

DT 06-MAY-2004 (first entry)

DE Mouse interleukin-1delta protein.

XX Interleukin-1zeta; gene therapy; immune system; haematopoietic cell;
 KW inflammatory disorder; infection; allergy; cancer; mouse.

OS Mus musculus.

PN US6680380-B1.

PD 20-JAN-2004.

PF 17-SEP-1999; 99US-00398412.

PR 18-SEP-1998; 98US-0100948P.

XX (SCHE) SCHERING CORP.

PI Timans JC;

XX WPI; 2004-189656/18.

PT New nucleic acid molecules encoding mammalian interleukin-1 polypeptides,
 PT useful for diagnosing, preventing or treating diseases associated with
 PT abnormal expression of interleukin, e.g. inflammation, infection or
 PT cancer.

PS Disclosure; SEQ ID NO 13; 36pp; English.

CC The invention relates to an isolated or recombinant nucleic acid encoding

CC Interleukin-1zeta polypeptide. The invention is useful in gene therapy.
 CC The composition and methods are useful in diagnosing or treating
 CC degenerative or abnormal conditions which directly or indirectly involve
 CC development, differentiation or function, e.g. of the immune system
 CC and/or haematopoietic cells. The invention may also be used for
 CC preventing or treating other diseases or disorders associated with
 CC abnormal expression or triggering of response to the interleukin, such as
 CC inflammatory disorders, infection, allergies or cancer. The present
 CC sequence is mouse interleukin-1delta.

SQ Sequence 156 AA;

Query Match 100.0%; Score 156; DB 8; Length 156;
 Best Local Similarity 100.0%; Pred. No. 4.2e-159;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMVLSGALCFRMDKSLKVLVYHNNQLAGGLHAEKVIKGEISVVPNRALDASISPVYL 60
 DB 1 MMVLSGALCFRMDKSLKVLVYHNNQLAGGLHAEKVIKGEISVVPNRALDASISPVYL 60
 OY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120
 DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120
 OY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFYQCCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFYQCCD 156

RESULT 7
 ADO04688
 ID ADO04688 standard; protein; 156 AA.

AC ADO04688;

DT 29-JUL-2004 (first entry)

DE Mouse interleukin-1d.

XX Interleukin-1d; IL-1d; immune system; inflammatory reaction;
 KW immunological disorder; mouse.

OS Mus sp.

XX Location/Qualifiers

FT Key
 FT Misc-difference 16
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 32
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 48
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 64
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 80
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 96
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 112
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 128
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 144
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 156
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

PN US2004087766-A1.
XX
XX 06-MAY-2004.
PD
XX
XX 27-OCT-2003; 2003US-00694978.
PF
XX 18-SEP-1998; 98US-0100948P.
PR 17-SEP-1999; 99US-00398412.
XX
XX (TIMA/) TIMANS J C.
PA
XX Timans JC;
PI
XX WPI, 2004-374758/35.
DR
XX
XX
XX New isolated or recombinant interleukin-1 zeta polypeptide and related
PT reagents such as antibodies, useful for treating inflammatory disease and
PT as probes for diagnosing immunological disorders.
PS
XX Disclosure; SEQ ID NO 13; 42pp; English.
PS
XX The invention relates to interleukin-1 zeta polypeptide and
CC polynucleotide. The agonist or antagonist of the interleukin-1 zeta is
CC useful in modulating a cell that is involved in inflammatory response.
CC The peptide fragments of IL-1 zeta are useful in research and diagnostic
CC tools in the study of inflammatory reactions to antigenic challenge and
CC the development of more effective anti-inflammatory therapeutics.
CC Interleukin-1 zeta is useful in regulation and/or development of immune
CC system. A polynucleotide encoding IL-1 zeta is useful for detecting the
CC expression level of the polypeptide in a patient suspected of having an
CC immunological disorder. The present sequence is mouse interleukin-1d.
CC Note: The present sequence is shown in Sequence Listing and pages 6-7 of
CC the specification. However, the sequence given in sequence listing has
CC incomplete 3-letter codes for several amino acids.
SQ
XX
XX Sequence 156 AA;
SQ
Query Match 100.0%; Score 156; DB 8; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.2e-159;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMVLSGALCFPMKDSALKVLYLHNNQLAGLHAKEKVKGBEISVVPNRALDASLSPVIL 60
DB 1 MMVLSGALCFPMKDSALKVLYLHNNQLAGLHAKEKVKGBEISVVPNRALDASLSPVIL 60
QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYLGAESKSFIFYRRDMGLTSSFESAAYPGW 120
DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYLGAESKSFIFYRRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPPADQPVRLTQIPEDPAMDAPITDIFYFOOCD 156
DB 121 FLCTSPPADQPVRLTQIPEDPAMDAPITDIFYFOOCD 156
RESULT 8
ADQ98213
ID ADQ98213 standard; protein; 156 AA.
XX
XX ADQ98213;
AC
XX
XX 07-OCT-2004 (first entry)
DT
XX
XX Mouse TANGO-93.
DE
XX mouse; TANGO-93; asthma; graft-versus-host disease; rheumatoid arthritis;
KW psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis;
KW Crohn's disease; chronic myelogenous leukemia; cancer; liver disease;
KW Hodgkin's disease; osteoarthritis; Lyme disease; cachexia;
KW autoimmune disease; myasthenia gravis; autoimmune diabetes;
KW systemic lupus erythematosus.
XX
XX Mus sp.
OS
XX

PN US2004142420-A1.
XX
XX 22-JUL-2004.
PD
XX
XX 12-DEC-2003; 2003US-00734985.
PF
XX 07-AUG-1998; 98US-00131263.
PR 06-AUG-1999; 99US-00369693.
XX 29-APR-2002; 2002US-00134410.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Pan Y;
PI
XX WPI, 2004-579909/56.
DR N-PSDB; ADQ98212.
XX
XX
XX New isolated TANGO-93 nucleic acids and proteins, useful for diagnosing,
PT screening, or treating asthma, rheumatoid arthritis, psoriasis, Crohn's
PT inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's
PT disease, cancer, or liver disease.
PS
XX Claim 8; SEQ ID NO 2; 39pp; English.
PS
XX The invention relates to an isolated TANGO-93 nucleic acid. The nucleic
CC acids and polypeptides are useful for diagnosing, screening, or treating
CC disorders having an aberrant TANGO-93 activity or expression. Diseases
CC include asthma, graft-versus-host disease, rheumatoid arthritis,
CC psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis,
CC Crohn's disease, chronic myelogenous leukemia, cancer, liver disease,
CC Hodgkin's disease, osteoarthritis, Lyme disease, cachexia, or autoimmune
CC disease, e.g., myasthenia gravis, autoimmune diabetes, or systemic lupus
CC erythematosus. The present sequence represents the amino acid sequence of
CC mouse TANGO-93.
SQ
XX
XX Sequence 156 AA;
SQ
Query Match 100.0%; Score 156; DB 8; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.2e-159;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMVLSGALCFPMKDSALKVLYLHNNQLAGLHAKEKVKGBEISVVPNRALDASLSPVIL 60
DB 1 MMVLSGALCFPMKDSALKVLYLHNNQLAGLHAKEKVKGBEISVVPNRALDASLSPVIL 60
QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYLGAESKSFIFYRRDMGLTSSFESAAYPGW 120
DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYLGAESKSFIFYRRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPPADQPVRLTQIPEDPAMDAPITDIFYFOOCD 156
DB 121 FLCTSPPADQPVRLTQIPEDPAMDAPITDIFYFOOCD 156
RESULT 9
AAI96937
ID AAI96937 standard; protein; 155 AA.
XX
XX AAI96937;
AC
XX
XX 31-OCT-2000 (first entry)
DT
XX
XX Murine IL-1 receptor antagonist 3.
DE
XX mtl-1Ra3; interleukin-1 receptor antagonist-3; IL-1ip; osteopathic;
KW interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
KW anti-arthritis; antimicrobial; respiratory; anti-ischemic; vaccine;
KW dermatological; immunomodulatory; gastrointestinal; gene therapy.
XX
XX Mus sp.
OS
XX WO200039297-A2.
PN
XX

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PD 06-JUN-2000.
XX
XX 22-DEC-1999; 99WO-US030720.
XX
XX 23-DEC-1998; 98US-0113430P.
XX 22-JAN-1999; 99US-011643P.
XX 13-APR-1999; 99US-0129122P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Goddard A, Pan J;
XX
XX WPI, 2000-452395/39.
XX DR N-PSDB; AAA51599.
XX
XX Nucleic acids encoding interleukin-1-like polypeptides, useful for
XX preventing and treating e.g. inflammation, asthma and psoriasis.
XX
XX Claim 22; Fig 9A-B; 143pp; English.
XX
XX An isolated nucleic acid molecule encoding an interleukin-1-like
XX polypeptide (IL-11p) that retains one or more activities of the peptide
XX from which it is derived, such as the IL-18R binding activity of a human
XX interleukin-1 receptor antagonist-1 (IL-1Ra1) polypeptide, is new. The
XX nucleic acids may be used in molecular engineering applications, e.g.
XX hybridization assays and chromosome and gene mapping studies, for
XX recombinantly producing the IL-11p polypeptide or for producing gene
XX knock out animals to study the role of the protein in metabolism and
XX disease processes (conversely, gene therapy protocols may be used to
XX supplement a patient's production of the polypeptide or to rectify
XX mutations that lead to the production of an active peptide). The
XX peptides produced may be used to screen for and produce modulators (e.g.
XX antibodies) of IL-11p protein expression and activity which may be used
XX to treat disorders associated with inappropriate IL-11p expression and
XX activity, such as inflammatory disorders, asthma, arthritis,
XX osteoarthritis, sepsis, acute lung injury, adult respiratory distress
XX syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
XX psoriasis, graft versus host disease and/or inflammatory bowel disease
XX
XX Sequence 155 AA;
XX
XX Query Match 99.4%; Score 155; DB 3; Length 155;
XX Best Local Similarity 100.0%; Pred. No. 5e-158;
XX Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 MYLGGALCFRMDKDALKVLVYHNNQLAGGLHAERKVIKGEISVVPNRALDASLSPVILG 61
XX DB 1 MYLGGALCFRMDKDALKVLVYHNNQLAGGLHAERKVIKGEISVVPNRALDASLSPVILG 60
XX
XX QY 62 VGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGMF 121
XX DB 61 VGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGMF 120
XX
XX QY 122 LCTSPBADQPVRLTQIPEDPAMDAPITDFYQOCD 156
XX DB 121 LCTSPBADQPVRLTQIPEDPAMDAPITDFYQOCD 155
XX
XX RESULT 10
XX AAB66672
XX ID AAB66672 standard; protein, 155 AA.
XX
XX AAB66672;
XX
XX 05-APR-2001 (first entry)
XX
XX Invention related sequence #4.
XX
XX Interleukin, IL-1 receptor; cancer; inflammation.
XX
XX Mus sp.
XX
XX WO200102571-A2.

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XX
XX 11-JAN-2001.
XX
XX 07-JUL-2000; 2000WO-US018710.
XX
XX 07-JUN-1998; 99US-00348942.
XX 13-OCT-1999; 99US-00417455.
XX 08-DEC-1999; 99US-00457626.
XX 10-MAR-2000; 2000US-00523552.
XX 22-MAY-2000; 2000US-00576008.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Ford J, Pace A;
XX
XX WPI, 2001-071582/08.
XX
XX Isolated nucleic acids encoding interleukin-1 (IL-1) receptor antagonist
XX proteins (referred as IL-1Hyl), useful in the treatment of cancer, e.g.
XX breast adenocarcinoma and brain tumors, and an inflammatory disease
XX mediated by IL-18.
XX
XX Disclosure; Page 177; 179pp; English.
XX
XX The present invention relates to interleukin (IL)-1 receptor antagonist
XX proteins. IL-1Hyl is useful for treating cancer, an inflammatory disease
XX mediated by IL-18, inflammation resulting from infection or allergic
XX reactions, and inflammation associated with chronic bronchitis,
XX arthritis, diabetes or endothermia
XX
XX Sequence 155 AA;
XX
XX Query Match 99.4%; Score 155; DB 4; Length 155;
XX Best Local Similarity 100.0%; Pred. No. 5e-158;
XX Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 MYLGGALCFRMDKDALKVLVYHNNQLAGGLHAERKVIKGEISVVPNRALDASLSPVILG 61
XX DB 1 MYLGGALCFRMDKDALKVLVYHNNQLAGGLHAERKVIKGEISVVPNRALDASLSPVILG 60
XX
XX QY 62 VGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGMF 121
XX DB 61 VGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGMF 120
XX
XX QY 122 LCTSPBADQPVRLTQIPEDPAMDAPITDFYQOCD 156
XX DB 121 LCTSPBADQPVRLTQIPEDPAMDAPITDFYQOCD 155
XX
XX RESULT 11
XX AAB48828
XX ID AAB48828 standard; protein, 155 AA.
XX
XX AAB48828;
XX
XX 09-MAR-2001 (first entry)
XX
XX Murine interleukin-1 homologue 3 (IL-1H3).
XX
XX Interleukin-1 homologue 3; IL-1H3; mouse; murine; drug screening;
XX agonist; antagonist; human disease; chronic inflammation;
XX acute inflammation; septicemia; autoimmune disease; psoriasis;
XX inflammatory bowel disease; arthritis; transplant rejection; infection;
XX graft versus host disease; acute respiratory distress syndrome; allergy;
XX asthma; restenosis; stroke; ischaemia; brain injury; AIDS; bone disease;
XX osteoporosis; cancer; lymphoproliferative disorder; atherosclerosis;
XX congestive heart failure; Alzheimer's disease; immunosuppressive;
XX antimicrobial; neuroprotective.
XX
XX Mus musculus.
XX
XX WO200071583-A1.

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PD 30-NOV-2000.
 XX 24-MAY-2000; 2000WO-US014200.
 XX 24-MAY-1999; 99US-0135599P.
 PR 23-MAY-2000; 2000US-00577715.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Smith RF, Young PR, McDonnell PC, Halsey W;
 XX WPI: 2001-025138/03.
 DR N-PSDB; AAC81700.
 XX Murine interleukin-1 homolog polypeptide used for screening modulators of
 PT the polypeptide which can be used for treating autoimmune diseases,
 PS cancer, brain injury and bone disorders.
 XX Claim 2; Page 28-29; 31pp; English.
 CC The invention relates to murine interleukin-1 homologue 3 (IL-1H3;
 CC AAB48828) and nucleic acid which encode it (cDNA given in AAC81700),
 CC including nucleic acid sequences with at least 95% identity to AAC81700.
 CC The invention also relates to expression vectors and host cells
 CC comprising murine IL-1H3 nucleic acids, the recombinant production of
 CC murine IL-1H3, methods of screening for modulators of IL-1H3 activity,
 CC and IL-1H3 agonists and antagonists thus identified. IL-1H3 agonists and
 CC antagonists are of use for treating human diseases such as chronic or
 CC acute inflammation, septicemia, autoimmune diseases (e.g., inflammatory
 CC bowel disease, psoriasis and arthritis), transplant rejection, graft
 CC versus host disease, infection, stroke, ischaemia, acute respiratory
 CC distress syndrome, allergies, asthma, restenosis, brain injury, AIDS,
 CC bone diseases (e.g., osteoporosis), cancers (e.g., lymphoproliferative
 CC disorders), congestive heart failure, atherosclerosis and Alzheimer's
 CC disease. The present sequence represents murine IL-1H3
 XX
 SQ Sequence 155 AA;
 Query Match 99.4%; Score 155; DB 4; Length 155;
 Best Local Similarity 100.0%; Pred. No. 5e-158;
 Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MVLGALCFPMKDSALKVLYLHNNQLAGGLHAKEVTKGEISVVPNRALDASLPVILG 61
 DB 1 MVLGALCFPMKDSALKVLYLHNNQLAGGLHAKEVTKGEISVVPNRALDASLPVILG 60
 QY 62 VGGSGQCLSCGTEKGPILKLEPNVIMELYGAKESKSFYRRDMGLTSSPESAAYPGW 121
 DB 61 VGGSGQCLSCGTEKGPILKLEPNVIMELYGAKESKSFYRRDMGLTSSPESAAYPGW 120
 QY 122 LCTSPBADQPVRLTQIPEDPAMDAPTIDFYFOCD 156
 DB 121 LCTSPBADQPVRLTQIPEDPAMDAPTIDFYFOCD 155
 RESULT 12
 AAB35261
 ID AAB35261 standard; protein; 155 AA.
 XX
 AC AAB35261;
 XX
 DT 08-MAY-2001 (first entry)
 XX
 DE Murine IL-1L1.
 XX
 KM Mouse; IL-1L1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;
 KM chromosome 2q13; inflammatory disease; heart disease; Graves' disease;
 KM rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;
 KM osteoporosis; systemic lupus erythematosus.
 XX
 OS Mus sp.
 XX

PN W0200105974-A2.
 XX 25-JAN-2001.
 PD
 XX 17-JUL-2000; 2000WO-US019508.
 PF
 XX 16-JUL-1999; 99US-0144298P.
 PR (INTE-) INTERLEUKIN GENETICS INC.
 XX
 PA Nicklin M, Barton J;
 XX WPI: 2001-091974/10.
 DR Nucleic acids encoding human and murine interleukin-1L1 polypeptides
 PT useful for controlling inflammatory processes.
 PS Claim 11; Fig 3; 150pp; English.
 CC The present invention provides the protein and coding sequences of the
 CC human and murine interleukin-1L1 (IL-1L1) proteins. The IL-1L1 gene is
 CC located between the IL-1beta and IL-1receptor genes at human chromosome
 CC 2q13. The sequences are useful in the diagnosis, prevention and treatment
 CC of heart disease, cancer and inflammatory diseases such as rheumatoid
 CC arthritis, systemic lupus erythematosus, inflammatory bowel disorder,
 CC diabetes, psoriasis, osteoporosis, lichen sclerosus, ulcerative colitis,
 CC severe periodontal disease and pregnancy complications. The present
 CC sequence is the murine IL-1L1 protein
 XX
 SQ Sequence 155 AA;
 Query Match 99.4%; Score 155; DB 4; Length 155;
 Best Local Similarity 100.0%; Pred. No. 5e-158;
 Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MVLGALCFPMKDSALKVLYLHNNQLAGGLHAKEVTKGEISVVPNRALDASLPVILG 61
 DB 1 MVLGALCFPMKDSALKVLYLHNNQLAGGLHAKEVTKGEISVVPNRALDASLPVILG 60
 QY 62 VGGSGQCLSCGTEKGPILKLEPNVIMELYGAKESKSFYRRDMGLTSSPESAAYPGW 121
 DB 61 VGGSGQCLSCGTEKGPILKLEPNVIMELYGAKESKSFYRRDMGLTSSPESAAYPGW 120
 QY 122 LCTSPBADQPVRLTQIPEDPAMDAPTIDFYFOCD 156
 DB 121 LCTSPBADQPVRLTQIPEDPAMDAPTIDFYFOCD 155
 RESULT 13
 AAB06663
 ID AAB06663 standard; protein; 154 AA.
 XX
 AC AAB06663;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Mouse interleukin-1delta (IL-1delta) protein.
 XX
 KM Mouse; interleukin-1delta; IL-1delta; viruslike; hepatotropic; fever;
 KM immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
 KM autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
 KM psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
 XX
 OS Mus sp.
 XX
 PN W0200157219-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 01-FEB-2001; 2001WO-US003285.
 XX
 PR 02-FEB-2000; 2000US-0179638P.
 XX

PA (SCHE) SCHERING CORP.
 XX Debets JEMA, Timans JC, Bazan JF, Kastelein RA;
 XX WPI, 2001-488886/53.
 DR Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
 PT polypeptide useful for treating conditions exhibiting abnormal expression
 PT of interleukin such as immunological disorders, tumor and allergy.
 XX
 PS Disclosure; Fig 1; 103pp; English.
 XX
 XX The invention relates to recombinant antigenic interleukin-1 like
 CC molecules and their corresponding nucleic acid sequences, designated as
 CC interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon). IL
 CC -1delta and IL-1epsilon are useful for treating conditions exhibiting
 CC abnormal expression of the interleukin such as immunological disorders,
 CC tumors, inflammatory disorders, fever, hypoglycaemia, psoriasis,
 CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
 CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
 CC HIV). The invention also relates to methods of using the composition
 CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
 CC utilities. IL-1delta is used as an immunogen for the production of
 CC antisera or antibodies specific, e.g., capable of distinguishing between
 CC IL-1 family members and an IL-1delta, for the interleukin or its
 CC fragment. The purified interleukin is used as a reagent to detect any
 CC antibodies generated in response to the presence of elevated levels of
 CC expression, or immunological disorders which lead to antibody production
 CC to the endogenous cytokine. The invention also contemplates the use of
 CC competitive drug screening assays. The present sequence is mouse
 CC interleukin-1delta (IL-1delta) protein related to the invention
 SQ Sequence 154 AA;
 Query Match 98.7%; Score 154; DB 4; Length 154;
 Best Local Similarity 100.0%; Pred. No. 5.9e-157; Indels 0; Gaps 0;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 VLSGALCFPMKDSALKVLYLHNNQLLAGLHAERIVKGEISVVPNRALDASLPVILGV 62
 DB 1 VLSGALCFPMKDSALKVLYLHNNQLLAGLHAERIVKGEISVVPNRALDASLPVILGV 60
 QY 63 QGSGOCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMDGLTSSFESAAYPGWFL 122
 DB 61 QGSGOCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMDGLTSSFESAAYPGWFL 120
 QY 123 CTSPEADQPVRLTQIPEDPAMDAPIITDFYFOOD 156
 DB 121 CTSPEADQPVRLTQIPEDPAMDAPIITDFYFOOD 154
 RESULT 14
 ABP52012
 ID ABP52012 standard; protein; 146 AA.
 AC ABP52012;
 XX
 XX 10-OCT-2002 (first entry)
 DT
 XX
 DE NOVINTRA A homologous amino acid sequence SEQ ID NO:55.
 XX
 XX Human; transmembrane protein; neuromedin protein; gonadotropin protein;
 KW interleukin-1 receptor antagonist; interleukin-1 epsilon; NOV;
 KW IL-1 epsilon; IL-1 receptor antagonist; lung disease; neutropenic;
 KW cytotoxic; neuroprotective; antiinflammatory; antibacterial;
 KW immunosuppressive; cerebroprotective; antidiabetic; antiarthritic;
 KW antiaesthetic; antiallergic; gene therapy; antibody-based therapy;
 KW cell signalling disorder; haematopoietic disorder; endocrine; muscle;
 KW neurodegenerative disorder; neurolgical disorder; cancer; melanoma;
 KW central nervous system cancer; reproductive development disorder; asthma;
 KW metabolic function disorder; bone metabolism structure disorder; stroke;
 KW inflammatory response disorder; immune regulation disorder; septic shock;
 KW diabetes; arthritis; lung cancer; emphysema; allergic lung irritation;

KW lung inflammation.
 XX Homo sapiens.
 OS
 XX US2002068279-A1.
 PN
 XX 06-JUN-2002.
 PD
 XX 05-DEC-2000; 2000US-00730617.
 PF
 XX 06-DEC-1999; 99US-0169056P.
 PR 09-DEC-1999; 99US-0169866P.
 PR 09-DEC-1999; 99US-0169866P.
 PR 10-DEC-1999; 99US-0170252P.
 PR 12-JAN-2000; 2000US-0175740P.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX Burgess C, Prayaga SK, Shimkets RA, Rastelli L, Zernusen B;
 PI Mezes P;
 DR WPI, 2002-582472/62.
 XX
 XX New NOVX proteins for diagnosing or treating cell signaling, immune
 PT response, hematopoietic, neurodegenerative, muscle, endocrine, bone, and
 PT reproductive development disorders.
 PS Disclosure; Fig 10B; 110pp; English.
 XX
 XX The present invention describes an isolated NOVX polypeptide, chosen from
 CC human transmembrane (NOVTRAN), neuromedin (NOVNEUR), gonadotropin
 CC (NOVGON), interleukin-1 (IL-1) receptor antagonist (NOVINTRA A and B),
 CC and IL-1 epsilon proteins. NOVX polypeptides have neutropenic, cytotoxic,
 CC neuroprotective, antiinflammatory, antibacterial, immunosuppressive,
 CC cerebroprotective, antidiabetic, antiarthritic, antiaesthetic and
 CC antiallergic activities, and can be used in gene therapy and antibody-
 CC based therapy. NOVX polypeptides, nucleic acid (I) encoding them and an
 CC antibody (III) that binds the polypeptide, are useful for treating or
 CC preventing a NOVX protein-associated disorder in humans. NOVTRAN can be
 CC used in the treatment of a cell signalling disorder, such as, a
 CC haematopoietic disorder or a neurodegenerative disorder. NOVNEUR can be
 CC used in the treatment of an endocrine, muscle, neurological disorder,
 CC central nervous system cancer, breast, colon, ovarian, kidney, prostate
 CC or thyroid cancer. NOVGO can be used in the treatment of a reproductive
 CC development disorder, metabolic function disorder or melanoma. NOVINTRA
 CC proteins can be used in the treatment of and a bone metabolism or
 CC structure disorder, an inflammatory response disorder, an immune
 CC regulation disorder, septic shock, stroke, diabetes, arthritis or cancer.
 CC An agent which modulates the expression or activity of a human IL-1
 CC epsilon protein is useful for treating a lung disease such as lung
 CC cancer, asthma, emphysema, allergic lung irritation and lung inflammation
 CC in a mammal. ABQ73996 to ABQ74027 and ABP51981 to ABP52048 represent
 CC sequences used in the exemplification of the present invention
 XX
 SQ Sequence 146 AA;
 Query Match 93.6%; Score 146; DB 5; Length 146;
 Best Local Similarity 100.0%; Pred. No. 2.3e-148; Indels 0; Gaps 0;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 CFRMDSALKVLYLHNNQLLAGLHAERIVKGEISVVPNRALDASLPVILGVGGSGCC 68
 DB 1 CFRMDSALKVLYLHNNQLLAGLHAERIVKGEISVVPNRALDASLPVILGVGGSGCC 60
 QY 69 LSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMDGLTSSFESAAYPGWFLCTSPEA 128
 DB 61 LSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMDGLTSSFESAAYPGWFLCTSPEA 120
 QY 129 DQPVRLTQIPEDPAMDAPIITDFYFOO 154
 DB 121 DQPVRLTQIPEDPAMDAPIITDFYFOO 146

Search completed: April 5, 2006, 15:10:21
Job time : 82 secs

```

RESULT 15
AA97068
ID AAY97068 standard; protein, 94 AA.
XX
XX AC AAY97068;
XX
XX DT 31-OCT-2000 (first entry)
XX
DE Murine IL-1 receptor antagonist 3 EST W08205 product.
XX
XX mIL-1Ra3; interleukin-1 receptor antagonist-3; IL-1p; osteopathic;
XX interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
XX anti-arthritic; antimicrobial; respiratory; anti-ischemic; vaccine;
XX dermatological; immunomodulatory; gastrointestinal; gene therapy.
XX
OS Mus sp.
XX
XX PN WO200039297-A2.
XX
XX PD 06-JUL-2000.
XX
XX PF 22-DEC-1999; 99WO-US030720.
XX
XX PR 23-DEC-1998; 98US-0113430P.
XX PR 22-JAN-1999; 99US-0116843P.
XX PR 13-APR-1999; 99US-0129122P.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Goddard A, Pan J;
XX
XX DR WPI; 2000-452395/39.
XX DR N-PSDB; AAA51600.
XX
XX PT Nucleic acid encoding interleukin-1-like polypeptides, useful for
XX PT preventing and treating e.g. inflammation, asthma and psoriasis.
XX
XX PS Example 1; Fig 10; 143pp; English.
XX
CC An isolated nucleic acid molecule encoding an interleukin-1-like
CC polypeptide (IL-1p) that retains one or more activities of the peptide
CC from which it is derived, such as the IL-18R binding activity of a human
CC interleukin-1 receptor antagonist-1 (hIL-1Ra1) polypeptide, is new. The
CC nucleic acids may be used in molecular engineering applications, e.g.
CC hybridization assays and chromosome and gene mapping studies, for
CC recombinantly producing the IL-1p polypeptide or for producing gene
CC knock out animals to study the role of the protein in metabolism and
CC disease processes (conversely, gene therapy protocols may be used to
CC supplement a patient's production of the polypeptide or to rectify
CC mutations that lead to the production of in active peptides). The
CC peptides produced may be used to screen for and produce modulators (e.g.
CC antibodies) of IL-1p protein expression and activity which may be use to
CC treat disorders associated with inappropriate IL-1p expression and
CC activity, such as inflammatory disorders, asthma, arthritis,
CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
CC psoriasis, graft versus host disease and/or inflammatory bowel disease
XX
SQ Sequence 94 AA;
Query Match 60.3%; Score 94; DB 3; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.3e-92;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMTLSGALCFRMDSAKLVLYLNNOQLAGLHAKEVYKGEESVVPNALDASLSPVIL 60
DB 1 MMTLSGALCFRMDSAKLVLYLNNOQLAGLHAKEVYKGEESVVPNALDASLSPVIL 60
QY 61 GVOGGSQCLSCGTEKGPILKLEPVNIMELYIAK 94
DB 61 GVOGGSQCLSCGTEKGPILKLEPVNIMELYIAK 94

```

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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:10:32 ; Search time 14 Seconds

(without alignments)
1072.130 Million cell updates/sec

Title: US-09-770-528-2

Perfect score: 156
Sequence: 1 MAMLSGALCFRMKDSALKVL.....IPEDPAMDAPITDFYFOQCD 156

Scoring table: OLIGO

Gapop 60.0 , Gapept 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 8

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 80.*

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 44 | 28.2 | 155 | 2 JC7104 | Interleukin-1 rece |
| 2 | 9 | 5.8 | 413 | 2 T05228 | hypothetical prote |
| 3 | 8 | 5.1 | 196 | 2 AH1149 | hypothetical prote |
| 4 | 8 | 5.1 | 196 | 2 A11508 | hypothetical prote |
| 5 | 8 | 5.1 | 883 | 2 T37208 | hypothetical prote |

ALIGNMENTS

RESULT 1

JC7104

Interleukin-1 receptor antagonist - human
C/Species: Homo sapiens (man)

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: JC7104

R/Mulero, J.J.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Ford, D.
Biochem. Biophys. Res. Commun. 263, 702-706, 1999

A/Title: IL1RL1: A novel Interleukin-1 receptor antagonist gene.

A/Reference number: JC7104; MUID:99443727; PMID:10512743

A/Accession: JC7104

A/Molecule type: mRNA

A/Residues: 1-155 <MULT>

A/Cross-references: UNIPROT:Q9UBH0; UNIPARC:UP10000034E98; GB:AF186094; NID:96049804; PI

C/Genetics:

A/Map position: 2q14

C/Keywords: macrophage

Query Match 28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 4.3e-39;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 LEPVIMELYLGAKEKSPFTYRRDMLTSSPSSAAYRGWFLCT 124
DB 80 LEPVIMELYLGAKEKSPFTYRRDMLTSSPSSAAYRGWFLCT 123

RESULT 2

T05228

hypothetical protein F1715.190 - Arabidopsis thaliana

N/Alternate names: hypothetical protein F28A23.240

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C/Accession: T05228; T05436

R/Bevan, M.; Vitale, D.; Ligouri, R.; Argitrou, A.; De Simone, V.; Hohnsbeil, J.; Mew

submitted to the Protein Sequence Database, July 1998

A/Reference number: Z15404

A/Accession: T05228

A/Molecule type: DNA

A/Residues: 1-413 <BEV>

A/Cross-references: UNIPROT:Q49504; UNIPARC:UP100000A0329; EMBL:AL031032

A/Experimental source: cultivar Columbia; BAC clone F1715

R/Bevan, M.; Weichselgartner, M.; Fattmann, B.; Grandérach, K.; Dauner, D.; Herzl, A.

submitted to the Protein Sequence Database, October 1998

A/Reference number: Z15415

A/Accession: T05436

A/Molecule type: DNA

A/Residues: 173-413 <BEV>

A/Cross-references: UNIPARC:UP1000017A66F; EMBL:AL021961

A/Experimental source: cultivar Columbia; BAC clone F28A23

C/Genetics:

A/Map position: 4

A/Intons: 306/3

A/Note: F1715.190; F28A23.240

Query Match 5.8%; Score 9; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ALDASLSPV 58
DB 356 ALDASLSPV 364

RESULT 3

AH1149

hypothetical protein lmo0600 [imported] - Listeria monocytogenes (strain EGD-e)

C/Species: Listeria monocytogenes

C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C/Accession: AH1149

R/Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entian, K.D.; Feibi,

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A/Authors: Kreft, J.; Kuhn, M.; Kunet, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.;

Ok, C.; Schlatterer, T.; Simoes, N.; Tixeret, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla

A/Title: Comparative genomics of Listeria species.

A/Reference number: AB1077; MUID:21537279; PMID:11679669

A/Accession: AH1149

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-196 <GLA>

A/Cross-references: UNIPROT:O8Y9D2; UNIPARC:UP1000005526; GB:NC_003210; PIDN:CAC9867

A/Experimental source: strain EGD-e

C/Genetics:

A/Map position: 5.1%; Score 8; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LSPVILGV 62
 |||||
 Db 130 LSPVILGV 137

RESULT 4

hypoetical protein lin0609 [imported] - Listeria innocua (strain Clp11262)
 A:Accession: A11508
 C:Species: Listeria innocua
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: A11508
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karsc, U.
 Science 294, 849-852, 2001
 A:Authors: Kref, J.; Kuhn, M.; Kunat, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; PMID:21537279; PMID:11679669
 A:Accession: A11508
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-196 <Glas>
 A:Cross-references: UNIPROT:Q92E52; UNIPARC:UPI00000CC2B8; GB:AL592022; PIDN:CAC95841.1;
 A:Experimental source: strain Clp11262
 C:Genetics:
 A:Gene: lin0609

Query Match 5.1%; Score 8; DB 2; Length 196;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LSPVILGV 62
 |||||
 Db 130 LSPVILGV 137

RESULT 5

T37208
 hypothetical protein Y57G7A.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T37208
 R:Ozerky, P.
 submitted to the EMBL Data Library, March 1999
 A:Description: The sequence of C. elegans cosmid Y57G7A.
 A:Reference number: Z21634
 A:Accession: T37208
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-883 <OZE>
 A:Cross-references: UNIPROT:O76623; UNIPARC:UPI0000076054; EMBL:AF077542; PIDN:AA26299.
 C:Genetics:
 A:Map position: II
 A:introns: 20/1; 47/1; 756/2; 822/2; 852/1
 A>Note: Y57G7A.6

Query Match 5.1%; Score 8; DB 2; Length 883;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 IMELYLGA 93
 |||||
 Db 231 IMELYLGA 238

Search completed: April 5, 2006, 15:10:54
 Job time : 14 secs

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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:09:00 ; Search time 77 Seconds

(without alignments)
1429.382 Million cell updates/sec

Title: US-09-770-528-2

Sequence: 1 MMVLGALCFRMKDSALKVL.....IPEDPAMDAPITDFYFOQCD 156

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 8

Total number of hits satisfying chosen parameters: 27

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------|---------------------|
| 1 | 156 | 100.0 | 156 | ILIF5_MOUSE | O99Y1 mus musculu |
| 2 | 44 | 28.2 | 155 | ILIF5_HUMAN | G9ubn0 h interleuk |
| 3 | 10 | | 104 | OSACR2_CANAL | Osacr2 candida alb |
| 4 | 9 | | 382 | OSTS48_ANOGA | OSTs48 anopheles g |
| 5 | 9 | | 413 | 049504_ARATH | 049504 arabidopsis |
| 6 | 9 | | 449 | 09C501_ARATH | 09C501 arabidopsis |
| 7 | 9 | | 454 | 09M703_ARATH | 09M703 arabidopsis |
| 8 | 8 | | 101 | 070AK0_XENTR | 070AK0 xenopus tro |
| 9 | 8 | | 110 | 070AK1_XENTR | 070AK1 xenopus lae |
| 10 | 8 | | 174 | ILIRA_BOVIN | 077482 bos taurus |
| 11 | 8 | | 196 | 08Y9D2_LISMO | 08Y9D2 listeria mo |
| 12 | 8 | | 196 | 092SE2_LISIN | 092SE2 listeria in |
| 13 | 8 | | 196 | 0722V0_LISIN | 0722V0 listeria mo |
| 14 | 8 | | 263 | 06B4C0_PETMA | 06B4C0 petromycon |
| 15 | 8 | | 278 | 06ETX4_ORYSA | 06ETX4 oryza sativ |
| 16 | 8 | | 397 | 0877R1_BACTIN | 0877R1 bacteroides |
| 17 | 8 | | 570 | 070AK2_XENTR | 070AK2 xenopus lae |
| 18 | 8 | | 581 | 09D505_MOUSE | 09D505 m mus muscu |
| 19 | 8 | | 590 | 09D254_MOUSE | 09D254 m mus muscu |
| 20 | 8 | | 620 | 04QF97_LEIMA | 04QF97 leishmania |
| 21 | 8 | | 637 | 06A073_MOUSE | 06A073 mus musculu |
| 22 | 8 | | 660 | FLR12_HUMAN | 043155 homo sapien |
| 23 | 8 | | 673 | 08BLU0_MOUSE | 08BLU0 mus musculu |
| 24 | 8 | | 673 | 07Y258_CHURE | 07Y258 chlamydomon |
| 25 | 8 | | 883 | 06X623_CABEL | 06X623 caenorhabdi |
| 26 | 8 | | 365 | 06XHA7_DICHI | 06XHA7 dictyoscelli |
| 27 | 8 | | 4780 | 05CRB3_CRYPY | 05CRB3 cryptospori |

ALIGNMENTS

RESULT 1
ID ILIF5_MOUSE STANDARD; PRT; 156 AA.
AC O99Y1; O9JIG2;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Interleukin 1 family member 5 (IL-1F5) (Interleukin-1 delta) (IL-1
DE delta) (Interleukin-1-like protein 1) (IL-1L1) (Interleukin-1 HX1)
DE (IL-1H1) (Interleukin-1 homolog 3) (IL-1H3).
GN Name: ILIF5; Synonyms: P11d, I11h3, I11h11,
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20545212; PubMed=11466363;
RX DeBets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
RA Kastelein R.A.;
RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
RT as an antagonist and agonist of NF-kappa B activation through the
RT orphan IL-1 receptor-related protein 2.";
RL Eur. J. Immunol. 167:1440-1446(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20545212; PubMed=11093146;
RX DOI=10.1002/1521-4141(200111)30:11<3299::AID-IMM3299>3.0.CO;2-S;
RA Barton J.L., Herbst R., Bossio D., Higgins L., Nicklin M.J.H.;
RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1
RT cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
RL Eur. J. Immunol. 30:3299-3308(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Timas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX STRAIN=C57BL/6J; TISSUE=Stomach; and Tongue;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1098/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,
RA Nakai K., Tomaru Y., Hasegawa Y., Nogi H., Yamada H., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogi H., Yamada H., Kiyosawa H.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kampen A., Matsuda H., Barilov S., Baisel K.W.,
RA Blake J.A., Brad T., Brusic V., Chotia C., Corbani L.E., Cousins S.,
RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimsmond S., Gustincich S., Hirokawa N., Jackson J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Malais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan M.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai K., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid D.J., Ring B.Z., Ringwald M.,
RA Savelkin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takemata Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Varadar R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynnham-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura N., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Aizawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kikawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RL 60,770 full-length cDNAs";
 Nature 420:563-573 (2002).
 (5)
 RN X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 3-156, AND DISULFIDE BOND.
 RP PubMed:12974628; DOI=10.1021/bi0341197;
 RA Dunn E.P., Gay N.J., Bristow A.F., Gearing D.P., O'Neill L.A.J.,
 RA Pei X.Y.;
 RT "High-resolution structure of murine interleukin 1 homologue IL-1F5
 RL reveals unique loop conformations for receptor binding specificity.";
 CC Biochemistry 42:10938-10944 (2003).
 CC -1- FUNCTION: Is a highly and a specific antagonist of the IL-1
 CC receptor-related protein 2-mediated response to interleukin 1
 CC family member 9 (IL1P9). Could constitute part of an independent
 CC signaling system analogous to interleukin-1 alpha (IL-1A), beta
 CC (IL-1B) receptor agonist and interleukin-1 receptor type I (IL-
 CC 1RI), that is present in epithelial barriers and takes part in
 CC local inflammatory response (By similarity).
 CC SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: Highly abundant in embryonic tissue and
 CC tissues containing epithelial cells.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AF2030378; AAF91275.1; -; mRNA.
 CC EMBL: AK009741; BAB26471.1; -; mRNA.
 CC EMBL: AK008977; BAB264002.1; -; mRNA.
 CC EMBL: AF2050429; CAB59831.1; ALT. INIT.; mRNA.
 CC EMBL: AF204955; AAF69251.1; -; mRNA.
 CC PDB: 1MD6; X-ray; A=3-156.
 CC DR Ensembl: ENSMUSG0000026983; Mus musculus.
 CC MGI: MGI:1859325; 11f5.
 CC InterPro: IPR0006975; Interleukin 1.
 CC InterPro: IPR003296; Interleukin1Lb.
 CC InterPro: IPR003297; Interleukin1LbA.
 CC PANTHER: PTHR10078:SF2; Interleukin1LbA; 1.
 CC Pfam: PF00340; IL1; 1.
 CC DR PRINTS: PRO0264; INTERLEUKIN1.
 CC DR PRINTS: PRO1359; INTERLEUKIN1B.
 CC DR PRINTS: PRO1360; INTERLEUKIN1X.
 CC DR PRODOM: PD002536; Interleukin_1; 1.
 CC DR SMART: SM00125; IL1; 1.
 CC DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 CC KW 3D-structure; Cytokine; Multigene family.
 CC FT DISULFID 9 155
 CC CONFLICT 2 152 Missing (in Ref. 3).
 CC SQ SEQUENCE 156 AA; 17136 MW; A4DIE2F93CF77A7 CRC64;
 Query Match 100.0%; Score 156; DB 1; Length 156;
 Best Local Similarity 100.0%; Pred. No. 3e-158;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID IL1F5_HUMAN STANDARD; PRT; 155 AA.
 AC OSUBHD; OS6AT9; O7RTZ6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 46, Last annotation update)
 DE Interleukin 1 family member 5 (IL-1F5) (Interleukin-1 delta) (IL-1
 DE delta) (F1L1 delta) (Interleukin-1-like protein 1) (IL-1L1)
 DE (Interleukin-1 HX1) (IL-1HX1) (Interleukin-1 receptor antagonist
 DE homolog 1) (IL-1ra homolog 1) (IL-1 related protein 3) (IL-1RP3).
 GN Name: IL1F5; Synonyms: F1L1D, IL1HX1, IL1L1, IL1RP3;
 GN ORFNames: UNQ1896/PRO4342;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 CC NCBI_Taxid=9606;
 CC (1)
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP TISSUE=Placenta;
 RC MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
 RX Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garika K.E.,
 RA Sims D.E.;
 RT "Four new members expand the IL-1 superfamily.";
 RL J. Biol. Chem. 275:1169-1175 (2000).
 (2)
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP TISSUE=Peril akin;
 RC MEDLINE=99443727; PubMed=10512743; DOI=10.1006/dbrc.1999.1440;
 RX Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
 RA Drmanac R., Ford J.E.;
 RT "IL1HY1: a novel interleukin-1 receptor antagonist gene";
 RL Biochem. Biophys. Res. Commun. 263:702-706 (1999).
 (3)
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP TISSUE=Placenta;
 RC MEDLINE=20545212; PubMed=11093146;
 RX DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMU3299>3.0.CO;2-S;
 RT Barton J.L., Herbst R., Bosio D., Higgins L., Nicklin M.J.H.;
 RL "A tissue specific IL-1 receptor antagonist homolog from the IL-1
 RL cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
 RL Eur. J. Immunol. 30:3299-3308 (2000).
 (4)
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP MEDLINE=21359532; PubMed=11466363;
 RX Debers R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
 RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
 RA Kastelein R.A.;
 RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
 RT as an antagonist and agonist of NF-kappa B activation through the
 RT orphan IL-1 receptor-related protein 2.";
 RL J. Immunol. 167:1440-1446 (2001).
 (5)
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RP MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184;
 RX Buefield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,
 RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;
 RT "Identification and gene organization of three novel members of the
 RT IL-1 family on human chromosome 2.";
 RL Genomics 66:213-216 (2000).
 (6)
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RP MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
 RX Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
 RA Kornman K.;
 RT "A sequence-based map of the nine genes of the human interleukin-1
 RT cluster.";
 RL Genomics 79:718-725 (2002).
 (7)
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RX Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,

RESULT 2
 IL1F5_HUMAN

RA Huang A., Kim H.S., Klimoweki L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh V., Smith V., Stinson J., Vagts A.,
RA Vanden R.L., Watanabe C., Wiedand D., Woods K., Xie M.-H.,
RA Yasuda D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "Type secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RT Genome Res. 13:2265-2270(2003).
RL [8]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT SER-47.
RA Rieder M.J., Johanson E.J., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Bertucci C.B., Wong M.W., Yi Q., Nickerson D.A.;
RT "SeattleSNPs: NHGRI HL66682 program for genomic applications. UW-
RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu/>).";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RL [9]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA PubMed15815621, DOI=10.1038/nature03466.
RA Hillier L.W., Graves T.A., Fulton R.S., Fulton L.A., Pepin K.H.,
RA Mix P., Wagner-McPherson C., Layman D., Wyllie K., Sekhon M.,
RA Becker M.C., Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E.,
RA Kremetzki C., Oddy L., Du H., Sun H., Bradshaw-Cordum H., Ali U.,
RA Carter J., Cordes M., Harris A., Isak A., van Brunt A., Nguyen C.,
RA Du P., Courtney U., Kallick J., Ozerky P., Abbott S., Armstrong J.,
RA Bellet E.A., Caruso L., Cedroni M., Cotton M., Davidson T., Desai A.,
RA Elliott G., Erb T., Fronick C., Gaike T., Hakenson W., Haglund K.,
RA Holmes A., Harkins R., Kim K., Kruchowski S.S., Strong K.M.,
RA Grewal N., Govea E., Hou S., Levy A., Martinka S., Mead C.,
RA McCellan M.D., Meyer R., Randall-Maher J., Tomlinson C.,
RA Dauphin-Kohlberg S., Szlinder J., Strong J.T., Thompson J., Yeakum M.,
RA Leonard S., Pearson C., Triani L., Radionenko M., Waligorski J.E.,
RA Wang C., Rock S.M., Tin-Wollam A.-M., Maupin R., Lattimore P.,
RA Wendt M.C., Yang S.-P., Pohl C., Wallis J.W., Spieth J., Bieri T.A.,
RA Bektovcic N., Nelson J.O., Osborne U., Ding L., Meyer R., Sabo A.,
RA Shokland Y., Sima P., Wohldmann P.E., Cook L.L., Hickendocham M.T.,
RA Elbert J., Williams D., Jones T.A., She X., Ciccarelli F.D.,
RA Izaurralde E., Taylor J., Schmitz J., Myers R.M., Cox D.R., Huang X.,
RA McCherson J.D., Mardis E.R., Clifton S.W., Warren W.C.,
RA Chmulla A.T., Eddy S.R., Marra M.A., Ocharenko I., Furey T.S.,
RA Miller W., Eichler E.E., Bork P., Suyama M., Torrents D.,
RA Waterston R.H., Wilson R.K.;
RT "Generation and annotation of the DNA sequences of human chromosomes 2
RT and 4.";
RL Nature 434:724-731(2005).
RL [10]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA TISSUE=Placenta;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marinina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshitsuki S., Carrinoni P., Prange C.,
RA Rata S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Borak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Is a highly and a specific antagonist of the IL-1
CC receptor-related protein 2-mediated response to interleukin 1

CC family member 9 (IL1P9). Could constitute part of an independent
CC signaling system analogous to interleukin-1 alpha (IL-1A), beta
CC (IL-1B) receptor agonist and interleukin-1 receptor type I (IL-
CC 1RI), that is present in epithelial barriers and takes part in
CC local inflammatory response.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Predominantly expressed in keratinocytes but
CC not in fibroblasts, endothelial cells or melanocytes. Detected
CC also in the spleen, brain leukocyte and macrophage cell types.
CC Increased in lesional psoriasis skin.
CC -1- INDUCTION: By phorbol ester (PMA) and lipopolysaccharide (LPS)
CC treatment in macrophage cell line.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AF201830; AAF25210.1; -; mRNA.
CC EMBL: AF186094; AAF02757.1; -; mRNA.
CC EMBL: AJ242737; CAB59822.1; -; mRNA.
CC EMBL: AJ242738; CAB59823.1; -; mRNA.
CC EMBL: AJ271338; CAB67704.1; -; Genomic DNA.
CC EMBL: AF216693; AAF76981.1; -; Genomic DNA.
CC EMBL: AF230377; AAF91274.1; -; mRNA.
CC EMBL: BN000002; CAD29877.1; -; Genomic DNA.
CC EMBL: AY359117; AAF59045.1; -; mRNA.
CC EMBL: AY329853; AAF59031.1; -; Genomic DNA.
CC EMBL: AC016724; AAY14990.1; -; Genomic DNA.
CC EMBL: BC024747; AAT4747.1; -; mRNA.
CC PIR: JC7104; JC7104.
CC HSSP: P18510; IL1R.
CC SMR: Q9UBH0; 2-155.
CC InRact: Q9UBH0; -
CC EMBL: ENSG00000136695; Homo sapiens.
CC HGNC: HGNC:15561; IL1F5.
CC DR: GO: 605507; -
CC DR: GO: 0005152; F: Interleukin-1 receptor antagonist activity; TAS.
CC DR: InterPro: IPR000975; Interleukin_1.
CC DR: InterPro: IPR003265; InterleukinIL1.
CC DR: InterPro: IPR003297; InterleukinIL1RA.
CC DR: PANTHER: PTHR10078:SF2; InterleukinIL1RA; 1.
CC DR: Pfam: PF00340; IL1; 1.
CC DR: PRINTS: PR00264; INTERLEUKIN1.
CC DR: PRINTS: PR01359; INTERLEUKIN1B.
CC DR: PRINTS: PR01360; INTERLEUKIN1X.
CC DR: ProDom: PD002536; Interleukin_1; 1.
CC DR: SMART: SM00125; IL1; 1.
CC DR: PROSITE: PS00253; INTERLEUKIN_1; 1.
CC KW Cytokine; Multigene family; Polymorphism.
CC FT Disulfid 8 154 By similarity.
CC FT VARIANT 47 47 N -> S.
CC -----
CC Query Match 28.2%; Score 44; DB 1; Length 155;
CC Best Local Similarity 100.0%; Pred. No. 2, 6e-38;
CC Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC Oy 81 LEPVIMELYLAKESKSPFYRRDGLTSSPSSAAYPGFLCT 124
CC DB LEPVIMELYLAKESKSPFYRRDGLTSSPSSAAYPGFLCT 123
CC -----
CC RESULT 3
CC OSACR2 CANAL PRELIMINARY; PRT; 104 AA.
CC AC OSACR2;
CC DT 10-MAY-2005 (TrEMBLrel. 30, Created)
CC DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
CC DE Hypothetical protein.
CC ORFNames=Ca019.7580;

OS Candida albicans SC5314.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=237561;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SC5314;
 RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
 RA Jones T., Federstepel N.A., Chibana H., Dungan J., Kalman S.,
 RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
 RA Davis R.W., Scherer S.;
 RL "The diploid genome sequence of Candida albicans."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SC5314;
 RA Dungan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegbola O.,
 RA Roberts J., Peterson K., Donnelly S., Favoretto S., Tsung K.-W.,
 RA Jones T., Scherer S., Agabian N.;
 RL "Annotation of the Genome of Candida albicans."
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL: AACQ0100032; EAL00454.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 104 AA; 11108 MW; 1879F070BE334FAB CRC64;
 OY 109 TSSFESAAYP 118
 DB 3 TSSFESAAYP 12
 Query Match 6.4%; Score 10; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 0.046;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 OSTS48 ANOGA PRELIMINARY; PRT; 382 AA.
 ID OSTS48 ANOGA PRELIMINARY; PRT; 382 AA.
 AC OSTS48;
 DT 01-FEB-2005 (TREMBLrel. 29, Created)
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE ENSANGP0000029593.
 GN ORFNames=ENSANGG0000022974;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RL The Anopheles gambiae re-annotation."
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL: AAB01008944; EAL40313.1; -; Genomic_DNA.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR003885; LRR_cyst.
 DR InterPro; IPR007092; LRR_SDS22.
 DR Pfam; PF00560; LRR_1; 3.
 DR PRINTS; PR00019; LEURICRPT.
 DR SMART; SM00365; LRR_SD22; 4.
 KW Leucine-rich repeat; Repeat.

SQ SEQUENCE 382 AA; 42611 MW; 97D4B319C1D9B647 CRC64;
 Query Match 5.8%; Score 9; DB 2; Length 382;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VLYLHNNQL 27
 DB 39 VLYLHNNQL 47
 Query Match 5.8%; Score 9; DB 2; Length 413;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 O49504 ARATH PRELIMINARY; PRT; 413 AA.
 ID O49504 ARATH PRELIMINARY; PRT; 413 AA.
 AC O49504;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE BZIP transcription factor-like protein.
 GN Name=FIT5.190; Synonyms=At4g34000;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Magnoliophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Bevan M., Vitale D., Liguori R., Argiriou A., De Simone V.,
 RA Honisel J., Mewes H.W., Mayer K.F.X., Schueller C.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Vitale D., Liguori R., Argiriou A., De Simone V., Mewes H.W.,
 RA Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE OF 162-306 AND 307-413.
 RA Weichselgattner M., Partmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031032; CAI19882.1; -; Genomic_DNA.
 DR EMBL; AL161584; CAB80117.1; -; Genomic_DNA.
 DR PIR; T05228; T05228.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; R:DNA binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR004827; TF_BZIP.
 DR PROSITE; PS00036; BZIP_BASIC; 1.
 SQ SEQUENCE 413 AA; 44666 MW; C05884DFD45EDD16 CRC64;

Query Match 5.8%; Score 9; DB 2; Length 413;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 ALDASLSPV 58
 DB 356 ALDASLSPV 364
 Query Match 5.8%; Score 9; DB 2; Length 449 AA.
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 O9C501 ARATH PRELIMINARY; PRT; 449 AA.
 ID O9C501 ARATH PRELIMINARY; PRT; 449 AA.
 AC O9C501 ARATH PRELIMINARY; PRT; 449 AA.
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

```

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE BZIP protein DBP5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN
RP NUCLEOTIDE SEQUENCE.
RA Kim S., Ma J., Li Z., Thomas T.L.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF34210; AAK19603.1; -; mRNA.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR011616; bzip 1.
DR InterPro: IPR004827; TF bzip.
DR Pfam: PF00170; bzip 1; 1.
DR SMART: SM00338; BRLZ; 1.
DR PROSITE: PS50217; BZIP 1.
DR PROSITE: PS00036; BZIP_BASIC; 1.
DR DNA-binding; Nuclear protein.
KW
SQ SEQUENCE 449 AA; 48905 MW; 79B7B6B4739872B9 CRC64;

Query Match 5.8%; Score 9; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 ALDASLSPV 58
DB 346 ALDASLSPV 354

RESULT 7
O9MT03 ARATH PRELIMINARY; PRT; 454 AA.
AC O9MT03.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Abscisic acid responsive elements-binding factor (Hypothetical protein
DE F1715.190:F1715.200) (ABRAB/FAP3).
GN Name=ABRAB; Synonyms=At4g34000, F1715.190:F1715.200;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=20102680; PubMed=1063668; DOI=10.1074/jbc.275.3.1723;
RA Choi H.-I., Hong J.-H., Ha J.-O., Kang J.-Y., Kim S.Y.;
RL "ABRAB, a family of ABA-responsive element binding factors.";
RT J. Biol. Chem. 275:1723-1730(2000).
RN
RP NUCLEOTIDE SEQUENCE.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinzaki K.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinzaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN
RP NUCLEOTIDE SEQUENCE.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinzaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
[4]

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RP NUCLEOTIDE SEQUENCE.
RA Tokoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
RA Narusaka M., Shinn P., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinzaki K.;
RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF093546; AAF27181.1; -; mRNA.
DR EMBL: AY054605; AAK96796.1; -; mRNA.
DR EMBL: AY081467; AAM10029.1; -; mRNA.
DR EMBL: AK175851; BAD43614.1; -; mRNA.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR011616; bzip 1.
DR InterPro: IPR004827; TF bzip.
DR Pfam: PF00170; bzip 1; 1.
DR SMART: SM00338; BRLZ; 1.
DR PROSITE: PS50217; BZIP 1.
DR PROSITE: PS00036; BZIP_BASIC; 1.
DR DNA-binding; Hypothetical protein; Nuclear protein.
KW
SQ SEQUENCE 454 AA; 49677 MW; B0428D39183374E9 CRC64;

Query Match 5.8%; Score 9; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 ALDASLSPV 58
DB 346 ALDASLSPV 354

RESULT 8
O70AKO XENTR PRELIMINARY; PRT; 101 AA.
AC O70AKO.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fibronectin leucine rich transmembrane protein 2 (Fragment).
GN Name=flectr;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN
RP NUCLEOTIDE SEQUENCE.
RA Boettcher R.T., Pollet N., Delius H., Niehrs C.;
RT "The transmembrane protein XFLRT3 forms a complex with FGF receptors
RT and promotes FGF signalling.";
RL Nat. Cell Biol. 6:38-44(2004).
DR EMBL: AJ605779; CAES4089.1; -; mRNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR001211; PhospholipaseA2.
DR Pfam: PF01462; LRRNT; 1.
DR SMART: SM00013; LRRNT; 1.
DR PROSITE: PS00119; PA2_ASP; UNKNOWN_1.
KW Transmembrane.
FT NON TER 101
SQ SEQUENCE 101 AA; 11296 MW; 27B6A6FC92AE01B1 CRC64;

Query Match 5.1%; Score 8; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VLYIHHNQ 26
DB 67 VLYIHHNQ 74

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RESULT 9
Q70AK1_XENLA PRELIMINARY; PRT; 110 AA.
ID Q70AK1;
AC Q70AK1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DR 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin leucine rich transmembrane protein 2 (Fragment).
GN Name=flrt2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8355;
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Boechter R.T., Pollet N., Delius H., Niehrs C.;
RT "The transmembrane protein XFLRT3 forms a complex with FGF receptors
and promotes FGF signalling.";
RL Nat. Cell Biol. 6:38-44(2004).
DR EMBL; AJ605778; CAES408.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000372; IPR_Nterm.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF01462; LRRT; 1.
DR SMART; SM00013; LRRT; 1.
DR PROSITE; PS00119; PA2_ASP; UNKNOWN_1.
KM Transmembrane.
FT NON TER 110
SQ SEQUENCE 110 AA; 1243 MW; F03922FC05D9DF0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 110;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 VLYVHNNQ 26
Db 67 VLYVHNNQ 74

RESULT 10
IL1RA_BOVIN STANDARD; PRT; 174 AA.
ID IL1RA_BOVIN;
AC 077482;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DR 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (IRAP)
DE (IL1 inhibitor) (IL-1RN).
GN Name=IL1RN;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE; 96305607; PubMed=9643454; DOI=10.1016/S0165-2427(98)00099-3;
RA Katsura R., Fukuda T., Yamana H., Hagiwara K., Goto M., Obata Y.,
RA Yoshino T., Iwai H.;
RT "Enzymatic amplification and expression of bovine interleukin-1
receptor antagonist cDNA.";
RL Vet. Immunol. Immunopathol. 62:197-208(1998).
DE FUNCTION: Inhibits the activity of IL-1 by binding to its
receptor. Has no IL-1 like activity.
DE SUBCELLULAR LOCATION: Secreted.
DE SIMILARITY: Belongs to the IL-1 family.

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removed.

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CC EMBL; AB005148; BAA31854.1; -, mRNA.
DR HSSP; P18510; 11LR.
DR SMR; 077482; 32-174.
DR InterPro; IPR000975; Interleukin_1.
DR InterPro; IPR003297; InterleukinIL1RA.
DR PANTHER; PTHR10078:SF2; InterleukinIL1RA; 1.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR PRINTS; PR01360; INTERLEUKIN1X.
DR PRODOM; PD002536; Interleukin_1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 174 Interleukin-1 receptor antagonist
FT FT protein.
FT CARBOHYD 107 107 N-linked (GlcNAc...) (Potential).
FT DISULFID 89 139 By similarity.
SQ SEQUENCE 174 AA; 1926 MW; 1B56E7F224FF051F CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 1; Length 174;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 PGMFLCTS 125
Db 140 PGMFLCTS 147

RESULT 11
Q8Y9D2_LISMO PRELIMINARY; PRT; 196 AA.
ID Q8Y9D2;
AC Q8Y9D2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DR 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lmo0600 protein.
GN Lmo0600 protein.
OS Ordered locus Names=Lmo0600;
OC Bacteria; Firmicutes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=EGD-e / Setovar 1/2a;
RC MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangeul L., Buchrieser C., Ruenick C., Amend A.,
RA Baquero F., Berche P., Biocher H., Brandt P., Chakraborty T.,
RA Charbit A., Cherouani F., Couve E., de Darvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fahi H., Garcia-del Portillo F., Garrido P., Jackson D.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapat G.,
RA Madueno E., Maitounam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstey G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Vose H., Weiland J., Cossart P.;
RA "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL591976; CAC9868.1; -, Genomic DNA.
DR PIR; AH1149; AH1149.
DR ListerList; LMO0600; -.
KW Complete proteome.
SQ SEQUENCE 196 AA; 22125 MW; EBB2F568F9C5EBB CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 196;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 LSPVILGV 62
Db 130 LSPVILGV 137

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RESULT 12
Q92E52_LISIN
ID Q92E52_LISIN PRELIMINARY; PRT; 196 AA.
AC Q92E52;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lin0609 protein.
GN OrderedLocustNames=lin0609;
OS Bacteria; Firmicutes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=1679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangeul L., Buchrieser C., Ruenick C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Chabdic A., Cherouti F., Couve E., de Darvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Eutian K.-D., Fslhi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Geobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurupkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng P., Nédjari H.,
RA Norrsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Furell R.,
RA Remmel B., Rose M., Schueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlund J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL, AL596165; CAC95841.1; -; Genomic_DNA.
DR PIR, A11508; A11508.
DR ListerList; LIN0609; -.
KW Complete proteome.
SQ SEQUENCE 196 AA; 2236 MW; 676734063FD3E9E1 CRC64;

Query Match 5.1%; Score 8; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LSPVILGV 62
DB 130 LSPVILGV 137

RESULT 13
Q722V0_LISMF
ID Q722V0_LISMF PRELIMINARY; PRT; 196 AA.
AC Q722V0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=IMOF2365_0629;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=265669;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15115801; DOI=10.1093/nar/gkh562;
RA Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Kolonay J.F., Raako D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beaman M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.U., Durkin A.S., Madupu R.,
RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Forberger H.A., Tran B., Katharopoulos L., Wondolowski L.D., Uhlrich G.A.,
RA Bayles D.O., Luchansky J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen Listeria monocytogenes reveal new insights into the core genome components of this species.";
RL Nucleic Acids Res. 32:2386-2395(2004).
DR EMBL, AB017324; AAT03411.1; -; Genomic_DNA.
DR TIGR; IMOF2365_0629; -.
KW Complete proteome; Hypothetical protein.

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SQ SEQUENCE 196 AA; 22059 MW; 55B5C6EBB58A9 CRC64;

Query Match 5.1%; Score 8; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LSPVILGV 62
DB 130 LSPVILGV 137

RESULT 14
Q6E4C0_PETWA
ID Q6E4C0_PETWA PRELIMINARY; PRT; 263 AA.
AC Q6E4C0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Variable lymphocyte receptor.
OS Petromyzon marinus (Sea Lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15241406; DOI=10.1038/nature02740;
RA Panzer Z., Amemiya C.T., Ehrhardt G.R., Cellin J., Larry Gartland G.,
RA Cooper M.D.;
RT "Somatic diversification of variable lymphocyte receptors in the agnathan sea lamprey.";
RL Nature 430:174-180(2004).
DR EMBL, AY578053; AAT70322.1; -; mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF01462; LRRNT_1.
DR Pfam; PF00560; LRR_1; 3.
DR PRINTS; PR00019; LEURICRPT.
DR SMART; SM00013; LRRNT_1.
DR SMART; SM00369; LRR_Typ; 3.
KW Receptor.
SQ SEQUENCE 263 AA; 28326 MW; D53ECAA7095F73 CRC64;

Query Match 5.1%; Score 8; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LYLNNOQL 27
DB 102 LYLNNOQL 109

RESULT 15
Q6ETX4_ORYSA
ID Q6ETX4_ORYSA PRELIMINARY; PRT; 278 AA.
AC Q6ETX4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative phospholipidyltransferase isomerase 1 (PAIL1).
GN Name=PO06C08.30;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, AP004683; BADD7896.1; -; Genomic_DNA.

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DR Gramene; Q6ETX4; -
 DR GO; GO:0016853; F:isomerase activity; IEA.
 DR GO; GO:0004640; F:phosphoribosylanthranilate isomerase activity; IEA.
 DR GO; GO:0006568; P:tryptophan metabolism; IEA.
 DR InterPro; IPR001240; PRAI.
 DR Pfam; PF00697; PRAI; 1.
 KW isomerase.
 SQ SEQUENCE 278 AA; 29698 MW; 9C5D8B8E3720C636 CRC64;

Query Match 5.1%; Score 8; DB 2; Length 278;
 Best Local Similarity 100.0%; Pred.No.16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LLAGGLHA 34
 |||||
 Db 223 LLAGGLHA 230

Search completed: April 5, 2006, 15:14:01
 Job time : 78 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:11:02 ; Search time 19 Seconds
(without alignments)
678.811 Million cell updates/sec

Title: US-09-770-528-2

Perfect score: 156
Sequence: I MMTLSGALCFRMDSALKVL.....IPEDPAMDAPITDPYFOQCD 156

Scoring table:

OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 8

Total number of hits satisfying chosen parameters: 40

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents AA:*
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3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 156 | 100.0 | 156 | 2 | US-09-398-412B-13 |
| 2 | 154 | 98.7 | 154 | 2 | US-09-775-046-11 |
| 3 | 44 | 28.2 | 80 | 2 | US-09-417-455-3 |
| 4 | 44 | 28.2 | 80 | 2 | US-09-348-942-3 |
| 5 | 44 | 28.2 | 80 | 2 | US-09-457-626-3 |
| 6 | 44 | 28.2 | 80 | 2 | US-09-576-008-3 |
| 7 | 44 | 28.2 | 155 | 2 | US-09-417-455-5 |
| 8 | 44 | 28.2 | 155 | 2 | US-09-348-942-5 |
| 9 | 44 | 28.2 | 155 | 2 | US-09-316-081-5 |
| 10 | 44 | 28.2 | 155 | 2 | US-09-578-458-5 |
| 11 | 44 | 28.2 | 155 | 2 | US-09-522-964A-5 |
| 12 | 44 | 28.2 | 155 | 2 | US-09-457-626-5 |
| 13 | 44 | 28.2 | 155 | 2 | US-09-576-008-5 |
| 14 | 44 | 28.2 | 155 | 2 | US-09-949-016-6827 |
| 15 | 44 | 28.2 | 155 | 2 | US-09-775-046-2 |
| 16 | 44 | 28.2 | 187 | 2 | US-09-949-016-9356 |
| 17 | 10 | 6.4 | 145 | 2 | US-09-248-796A-25019 |
| 18 | 9 | 5.8 | 454 | 2 | US-09-416-050A-6 |
| 19 | 9 | 5.8 | 454 | 2 | US-09-664-800-6 |
| 20 | 9 | 5.8 | 454 | 2 | US-09-665-109-6 |
| 21 | 9 | 5.8 | 454 | 2 | US-09-661-569-6 |
| 22 | 8 | 5.1 | 136 | 2 | US-09-647-224A-22 |
| 23 | 8 | 5.1 | 268 | 2 | US-09-647-224A-20 |
| 24 | 8 | 5.1 | 275 | 2 | US-09-647-224A-24 |
| 25 | 8 | 5.1 | 660 | 2 | US-09-794A-28 |
| 26 | 8 | 5.1 | 660 | 2 | US-09-905-125A-28 |
| 27 | 8 | 5.1 | 660 | 2 | US-09-902-775A-28 |

| | | | | | | |
|----|---|-----|-----|---|--------------------|-------------------|
| 28 | 8 | 5.1 | 660 | 2 | US-09-906-700-28 | Sequence 28, Appl |
| 29 | 8 | 5.1 | 660 | 2 | US-09-903-603A-28 | Sequence 28, Appl |
| 30 | 8 | 5.1 | 660 | 2 | US-09-904-920A-28 | Sequence 28, Appl |
| 31 | 8 | 5.1 | 660 | 2 | US-09-949-016-6843 | Sequence 6843, Ap |
| 32 | 8 | 5.1 | 660 | 2 | US-09-909-064-28 | Sequence 28, Appl |
| 33 | 8 | 5.1 | 660 | 2 | US-09-905-381A-28 | Sequence 28, Appl |
| 34 | 8 | 5.1 | 660 | 2 | US-09-906-618-28 | Sequence 28, Appl |
| 35 | 8 | 5.1 | 660 | 2 | US-09-906-646-28 | Sequence 28, Appl |
| 36 | 8 | 5.1 | 660 | 2 | US-09-689-486-58 | Sequence 58, Appl |
| 37 | 8 | 5.1 | 660 | 2 | US-09-904-462-28 | Sequence 28, Appl |
| 38 | 8 | 5.1 | 660 | 2 | US-09-902-736A-28 | Sequence 28, Appl |
| 39 | 8 | 5.1 | 660 | 2 | US-09-906-722A-28 | Sequence 28, Appl |
| 40 | 8 | 5.1 | 683 | 2 | US-09-949-016-7267 | Sequence 7267, Ap |

ALIGNMENTS

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RESULT 1
US-09-398-412B-13
; Sequence 13, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Titans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related re
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398, 412B
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-398-412B-13

Query Match          100.0%; Score 156; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 6.9e-154;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MMTLSGALCFRMDSALKVLTHNNOLLAGLHAERVIKGBISVVPNRALDASLSPVIL 60
DB      1 MMTLSGALCFRMDSALKVLTHNNOLLAGLHAERVIKGBISVVPNRALDASLSPVIL 60

QY      61 GVGGSQCISCGTEKGPILKLEPVNIMELYLGAKEKSPFFYRRDMGLTSSFFSAAYPGW 120
DB      61 GVGGSQCISCGTEKGPILKLEPVNIMELYLGAKEKSPFFYRRDMGLTSSFFSAAYPGW 120

QY      121 FLCTSPADQPVRLTOIPEDPAMDAPITDPYFOQCD 156
DB      121 FLCTSPADQPVRLTOIPEDPAMDAPITDPYFOQCD 156

RESULT 2
US-09-775-046-11
; Sequence 11, Application US/09775046
; Patent No. 6843987
; GENERAL INFORMATION:
; APPLICANT: Debets, Johannes Eduard Maria Antonius
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastlein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01073K
; CURRENT APPLICATION NUMBER: US/09/775, 046
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/179, 638
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
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; SEQ ID NO 11
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-775-046-11

Query Match      98.7%; Score 154; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.1e-152;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  VTSALCFPMKDSALVLYIHNNQLLAGGHAHAKVKGSEISVPPRALDASIPVILGV 62
        |||
        1  VTSALCFPMKDSALVLYIHNNQLLAGGHAHAKVKGSEISVPPRALDASIPVILGV 60
        |||
QY      63  OGGSGCLSGCTEGPTIKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAYPGWFL 122
        |||
        61  OGGSGCLSGCTEGPTIKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAYPGWFL 120
        |||
QY      123  CTSPEADQPVRLTQIPEDEPAMDAPITDFYFQOCD 156
        |||
        121  CTSPEADQPVRLTQIPEDEPAMDAPITDFYFQOCD 154
        |||

RESULT 3
US-09-417-455-3
; Sequence 3, Application US/09417455
; Patent No. 6294655
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36328
; CURRENT APPLICATION NUMBER: US/09/417,455
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-417-455-3

Query Match      28.2%; Score 44; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 5.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81  LEPVNIMELYGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 124
        |||
        5  LEPVNIMELYGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 48
        |||

RESULT 4
US-09-348-942-3

; Sequence 3, Application US/09348942
; Patent No. 6337072
; GENERAL INFORMATION:
; APPLICANT: John Ford
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36010
; CURRENT APPLICATION NUMBER: US/09/348,942
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-348-942-3

Query Match      28.2%; Score 44; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 5.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81  LEPVNIMELYGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 124
        |||
        5  LEPVNIMELYGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 48
        |||

RESULT 5
US-09-457-626-3
; Sequence 3, Application US/09457626
; Patent No. 6426191
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36010
; CURRENT APPLICATION NUMBER: US/09/457,626
; CURRENT FILING DATE: 1999-12-08
; EARLIER APPLICATION NUMBER: US 09/417,455
; EARLIER FILING DATE: 1999-10-13
; EARLIER APPLICATION NUMBER: US 09/348,942
; EARLIER FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
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; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-626-3

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Query Match      28.2%; Score 44; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 5,9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      81 LEPVNIMELYGAKESKSFYFRDMDGLTSSFESAAYPGWFLCT 124
Db      5 LEPVNIMELYGAKESKSFYFRDMDGLTSSFESAAYPGWFLCT 48

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RESULT 6
US-09-576-008-3
; Sequence 3, Application US/09576008
; Patent No. 6541623
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Ho, Alice Suk-ye
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36456
; CURRENT APPLICATION NUMBER: US/09/576,008
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/523,552
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/457,626
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 09/417,455
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-576-008-3

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Query Match      28.2%; Score 44; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 5,9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      81 LEPVNIMELYGAKESKSFYFRDMDGLTSSFESAAYPGWFLCT 124
Db      5 LEPVNIMELYGAKESKSFYFRDMDGLTSSFESAAYPGWFLCT 48

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RESULT 7
US-09-417-455-5
; Sequence 5, Application US/09417455
; Patent No. 6294655
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36328
; CURRENT APPLICATION NUMBER: US/09/417,455
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-417-455-5

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Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      81 LEPVNIMELYGAKESKSFYFRDMDGLTSSFESAAYPGWFLCT 124
Db      80 LEPVNIMELYGAKESKSFYFRDMDGLTSSFESAAYPGWFLCT 123

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RESULT 8
US-09-348-942-5
; Sequence 5, Application US/09348942
; Patent No. 6337072
; GENERAL INFORMATION:
; APPLICANT: John Ford
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/35801
; CURRENT APPLICATION NUMBER: US/09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364

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; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PateSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-348-942-5

Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 LEPVNIMELYLGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 124
DB      80 LEPVNIMELYLGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 123

RESULT 9
US-09-316-081-5
; Sequence 5, Application US/09316081
; Patent No. 6339141
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/35659
; CURRENT APPLICATION NUMBER: US/09/316,081
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-316-081-5

Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 LEPVNIMELYLGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 124
DB      80 LEPVNIMELYLGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 123

RESULT 10
US-09-578-458-5
; Sequence 5, Application US/09578458
; Patent No. 6365726
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Ford, John
; APPLICANT: Ho, Alice
; APPLICANT: Lin, Hai Shan
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/36479
; CURRENT APPLICATION NUMBER: US/09/578,458
; CURRENT FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/522,964
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/316,086
; PRIOR FILING DATE: 1999-03-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-578-458-5

Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 LEPVNIMELYLGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 124
DB      80 LEPVNIMELYLGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 123

RESULT 11
US-09-522-964A-5
; Sequence 5, Application US/09522964A
; Patent No. 6372892
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Pace, Ann M.
; APPLICANT: Lin, Hai Shan
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/36210
; CURRENT APPLICATION NUMBER: US/09/522,964A
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/316,086
; PRIOR FILING DATE: 1999-03-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-522-964A-5

Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 LEPVNIMELYLGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 124
DB      80 LEPVNIMELYLGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 123

RESULT 12
US-09-457-626-5
; Sequence 5, Application US/09457626
; Patent No. 6426191
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36010
; CURRENT APPLICATION NUMBER: US/09/457,626
; CURRENT FILING DATE: 1999-12-08
; EARLIER APPLICATION NUMBER: US 09/417,455
; EARLIER FILING DATE: 1999-10-13
; EARLIER APPLICATION NUMBER: US 09/348,942
; EARLIER FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
```

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/ EARLIER FILING DATE: 1998-05-15
/ EARLIER APPLICATION NUMBER: US 09/055,010
/ EARLIER FILING DATE: 1998-04-03
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 5
/ LENGTH: 155
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-457-626-5

Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 LEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGWFLCT 124
      80 LEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGWFLCT 123

RESULT 13
US-09-576-008-5
/ Sequence 5, Application US/09576008
/ Patent No. 6541623
/ GENERAL INFORMATION:
/ APPLICANT: Ford, John
/ APPLICANT: Ho, Alice Suk-yue
/ APPLICANT: Pace, Ann
/ TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
/ FILE REFERENCE: 28110/36456
/ CURRENT APPLICATION NUMBER: US/09/576,008
/ CURRENT FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: US 09/523,552
/ PRIOR FILING DATE: 2000-03-10
/ PRIOR APPLICATION NUMBER: US 09/457,626
/ PRIOR FILING DATE: 1998-12-08
/ PRIOR APPLICATION NUMBER: US 09/417,455
/ PRIOR FILING DATE: 1999-10-13
/ PRIOR APPLICATION NUMBER: US 09/348,942
/ PRIOR FILING DATE: 1999-07-07
/ PRIOR APPLICATION NUMBER: PCT/US99/04291
/ PRIOR FILING DATE: 1999-04-05
/ PRIOR APPLICATION NUMBER: US 09/287,210
/ PRIOR FILING DATE: 1999-04-05
/ PRIOR APPLICATION NUMBER: US 09/251,370
/ PRIOR FILING DATE: 1999-02-17
/ PRIOR APPLICATION NUMBER: US 09/229,591
/ PRIOR FILING DATE: 1998-01-13
/ PRIOR APPLICATION NUMBER: US 09/127,698
/ PRIOR FILING DATE: 1998-07-31
/ PRIOR APPLICATION NUMBER: US 09/099,818
/ PRIOR FILING DATE: 1998-06-19
/ PRIOR APPLICATION NUMBER: US 09/082,364
/ PRIOR FILING DATE: 1998-05-20
/ PRIOR APPLICATION NUMBER: US 09/079,909
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: US 09/055,010
/ PRIOR FILING DATE: 1998-04-03
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 5
/ LENGTH: 155
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-576-008-5

Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 LEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGWFLCT 124
      80 LEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGWFLCT 123
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RESULT 14
US-09-949-016-6827
/ Sequence 6827, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6827
/ LENGTH: 155
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-6827

Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 LEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGWFLCT 124
      80 LEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGWFLCT 123

RESULT 15
US-09-775-046-2
/ Sequence 2, Application US/09775046
/ Patent No. 6843987
/ GENERAL INFORMATION:
/ APPLICANT: Debets, Johannes Eduard Maria Antonius
/ APPLICANT: Timans, Jacqueline C.
/ APPLICANT: Bazan, J. Fernando
/ APPLICANT: Kaseleijn, Robert A.
/ TITLE OF INVENTION: MAMMALIAN CYTOKINES, RECEPTORS, RELATED REAGENTS AND METHODS
/ FILE REFERENCE: DX01073X
/ CURRENT APPLICATION NUMBER: US/09/775,046
/ CURRENT FILING DATE: 2001-02-01
/ PRIOR APPLICATION NUMBER: 60/179,638
/ PRIOR FILING DATE: 2000-02-02
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 155
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-775-046-2

Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 LEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGWFLCT 124
      80 LEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGWFLCT 123

Search completed: April 5, 2006, 15:11:28
Job time : 19 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 5, 2006, 15:11:37 ; Search time 45 Seconds
(without alignments)
1448.475 Million cell updates/sec

Title: US-09-770-528-2
Perfect score: 156
Sequence: 1 MMVLGALCFRMDSALKVL.....IPEDPAWDAPITDFPOCCD 156

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 8

Total number of hits satisfying chosen parameters: 766

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 156 | 100.0 | 156 | 3 | US-09-770-528-2 |
| 2 | 156 | 100.0 | 156 | 3 | US-09-965-640-2 |
| 3 | 156 | 100.0 | 156 | 4 | US-10-267-791-2 |
| 4 | 156 | 100.0 | 156 | 4 | US-10-042-865-124 |
| 5 | 156 | 100.0 | 156 | 4 | US-10-695-195-13 |
| 6 | 156 | 100.0 | 156 | 4 | US-10-694-978-13 |
| 7 | 156 | 100.0 | 156 | 4 | US-10-734-985-2 |
| 8 | 156 | 100.0 | 156 | 5 | US-10-948-820-2 |
| 9 | 155 | 99.4 | 155 | 4 | US-10-042-865-123 |
| 10 | 154 | 98.7 | 154 | 3 | US-09-775-046-11 |
| 11 | 146 | 93.6 | 146 | 3 | US-09-730-617-55 |
| 12 | 88 | 28.2 | 80 | 4 | US-10-205-821-1 |
| 13 | 44 | 28.2 | 143 | 4 | US-10-287-190-70 |
| 14 | 44 | 28.2 | 143 | 4 | US-10-287-190-76 |
| 15 | 44 | 28.2 | 146 | 3 | US-09-730-617-58 |
| 16 | 44 | 28.2 | 147 | 3 | US-09-730-617-76 |
| 17 | 44 | 28.2 | 147 | 4 | US-10-287-190-72 |
| 18 | 44 | 28.2 | 147 | 4 | US-10-287-190-72 |
| 19 | 44 | 28.2 | 155 | 3 | US-09-730-617-61 |
| 20 | 44 | 28.2 | 155 | 3 | US-09-730-617-80 |
| 21 | 44 | 28.2 | 155 | 3 | US-09-730-617-96 |
| 22 | 44 | 28.2 | 155 | 3 | US-09-775-046-2 |
| 23 | 44 | 28.2 | 155 | 3 | US-09-965-640-4 |
| 24 | 44 | 28.2 | 155 | 4 | US-10-006-867-152 |
| 25 | 44 | 28.2 | 155 | 4 | US-10-003-671A-5 |
| 26 | 44 | 28.2 | 155 | 4 | US-10-063-547-152 |
| 27 | 44 | 28.2 | 155 | 4 | US-10-063-551-152 |

| | | | | | | |
|----|----|------|-----|---|-------------------|-------------------|
| 28 | 44 | 28.2 | 155 | 4 | US-10-139-833-10 | Sequence 10, App1 |
| 29 | 44 | 28.2 | 155 | 4 | US-10-063-616-152 | Sequence 152, App |
| 30 | 44 | 28.2 | 155 | 4 | US-10-063-569-152 | Sequence 152, App |
| 31 | 44 | 28.2 | 155 | 4 | US-10-063-513-152 | Sequence 152, App |
| 32 | 44 | 28.2 | 155 | 4 | US-10-063-515-152 | Sequence 152, App |
| 33 | 44 | 28.2 | 155 | 4 | US-10-063-512-152 | Sequence 152, App |
| 34 | 44 | 28.2 | 155 | 4 | US-10-063-502-152 | Sequence 152, App |
| 35 | 44 | 28.2 | 155 | 4 | US-10-063-549-152 | Sequence 152, App |
| 36 | 44 | 28.2 | 155 | 4 | US-10-063-554-152 | Sequence 152, App |
| 37 | 44 | 28.2 | 155 | 4 | US-10-063-553-152 | Sequence 152, App |
| 38 | 44 | 28.2 | 155 | 4 | US-10-063-518-152 | Sequence 152, App |
| 39 | 44 | 28.2 | 155 | 4 | US-10-063-598-152 | Sequence 152, App |
| 40 | 44 | 28.2 | 155 | 4 | US-10-227-693-152 | Sequence 152, App |
| 41 | 44 | 28.2 | 155 | 4 | US-10-267-791-5 | Sequence 5, App1 |
| 42 | 44 | 28.2 | 155 | 4 | US-10-063-563-152 | Sequence 152, App |
| 43 | 44 | 28.2 | 155 | 4 | US-10-063-555-152 | Sequence 152, App |
| 44 | 44 | 28.2 | 155 | 4 | US-10-063-594-152 | Sequence 152, App |
| 45 | 44 | 28.2 | 155 | 4 | US-10-063-567-152 | Sequence 152, App |

ALIGNMENTS

RESULT 1
US-09-770-528-2
Sequence 2, Application US/09770528
Patent No. US20020164332A1
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
Sana, Theodore R.
Bazan, Fernando J.
Kastelein, Robert A.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,528
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/130,972
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/055,111
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: US 09/062,866
FILING DATE: 20-APR-1998
APPLICATION NUMBER: US 09/097,976
FILING DATE: 16-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0725K2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
FAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-770-528-2

Query Match 100.0%; Score 156; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.4e-145;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASISPVIL 60
DB 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASISPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSTFYRRDMGLTSSFESAAYPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSTFYRRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEBPAMDAPITDFFYQOCD 156
DB 121 FLCTSPBADQPVRLTQIPEBPAMDAPITDFFYQOCD 156

RESULT 2

US-09-965-640-2
Sequence 2, Application US/09965640
Publication No. US20020187122A1
GENERAL INFORMATION:
APPLICANT: Sims, John E.
TITLE OF INVENTION: IL-1 DELTA DNA AND POLYPEPTIDES
FILE REFERENCE: 0315-C
CURRENT APPLICATION NUMBER: US/09/965,640
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/612,921
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 156
TYPE: PRT
ORGANISM: Mus musculus
US-09-965-640-2

Query Match 100.0%; Score 156; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.4e-145;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASISPVIL 60
DB 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASISPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSTFYRRDMGLTSSFESAAYPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSTFYRRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEBPAMDAPITDFFYQOCD 156
DB 121 FLCTSPBADQPVRLTQIPEBPAMDAPITDFFYQOCD 156

RESULT 3

US-10-267-791-2
Sequence 2, Application US/10267791
Publication No. US20030059892A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF THE TANGO-93-RELATED PROTEIN FAMILY
FILE REFERENCE: 07334-200001 (formerly 09404/086001)
CURRENT APPLICATION NUMBER: US/10/267,791
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/369,693
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: US 09/331,263
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2

Query Match 100.0%; Score 156; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.4e-145;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASISPVIL 60
DB 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASISPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSTFYRRDMGLTSSFESAAYPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSTFYRRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEBPAMDAPITDFFYQOCD 156
DB 121 FLCTSPBADQPVRLTQIPEBPAMDAPITDFFYQOCD 156

RESULT 4

US-10-042-865-124
Sequence 124, Application US/10042865
Publication No. US20040029216A1
GENERAL INFORMATION:
APPLICANT: Padigar, Muralidhara
APPLICANT: Li, Li
APPLICANT: Zernusen, Bryan D
APPLICANT: Caeman, Steacie J
APPLICANT: Shenoy, Sureesh G
APPLICANT: Spytek, Kimberly
APPLICANT: Zhong, Mei
APPLICANT: Gangolli, Beha A
APPLICANT: Burgess, Catherine B
APPLICANT: Paturajan, Meera
APPLICANT: Verne, Corine A.M
APPLICANT: Taylor, Sarah
APPLICANT: Tcherev, Velizar T
APPLICANT: Miller, Charles E
APPLICANT: Guo, Xiaojia
APPLICANT: Boldog, Ference L
APPLICANT: Grose, William M
APPLICANT: Alsbrook II, John P
APPLICANT: Gerlach, Valerie L
APPLICANT: Edinger, Shlomit R
APPLICANT: Rothenberg, Mark E
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Malyankar, Uriel M
APPLICANT: Miller, Isabelle
APPLICANT: Peyman, John
APPLICANT: Smithson, Glenda
APPLICANT: Gunther, Erik
APPLICANT: Stone, David
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
FILE REFERENCE: 21402-537
CURRENT APPLICATION NUMBER: US/10/042,865
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/260,831
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 60/272,338
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/284,704
PRIOR FILING DATE: 2001-04-18

NUMBER OF SEQ ID NOS: 264
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 124
LENGTH: 156
TYPE: PRT
ORGANISM: Mus. musculus
US-10-042-865-124

Query Match 100.0%; Score 156; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.4e-145;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAKLVYLHNNQLAGLHAERKVTGSEISVVPNRALDASLSPVIL 60
DB 1 MMVLSGALCFRMDKSAKLVYLHNNQLAGLHAERKVTGSEISVVPNRALDASLSPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAYPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOOCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOOCD 156

RESULT 5

US-10-695-195-13
Sequence 13, Application US/10695195
Publication No. US20040068099A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/695,195
FILING DATE: 27-Oct-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/398,412
FILING DATE: 17-Sep-1999
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0904K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-695-195-13

Query Match 100.0%; Score 156; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.4e-145;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAKLVYLHNNQLAGLHAERKVTGSEISVVPNRALDASLSPVIL 60
DB 1 MMVLSGALCFRMDKSAKLVYLHNNQLAGLHAERKVTGSEISVVPNRALDASLSPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAYPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOOCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOOCD 156

RESULT 6

US-10-694-978-13
Sequence 13, Application US/10694978
Publication No. US2004008766A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/694,978
FILING DATE: 27-Oct-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/398,412
FILING DATE: 17-Sep-1999
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0904K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-694-978-13

Query Match 100.0%; Score 156; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.4e-145;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAKLVYLHNNQLAGLHAERKVTGSEISVVPNRALDASLSPVIL 60
DB 1 MMVLSGALCFRMDKSAKLVYLHNNQLAGLHAERKVTGSEISVVPNRALDASLSPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAYPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOOCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOOCD 156

RESULT 7
US-10-734-985-2
; Sequence 2, Application US/10734985
; Publication No. US20040142420A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TANGO-93-RELATED
; FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-369001
; CURRENT APPLICATION NUMBER: US/10/734,985
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US/10/134,410
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 09/131,263
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: US 09/369,693
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-734-985-2

Query Match 100.0%; Score 156; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.4e-145;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MMTLSGALCFRMDKDALKVLTLHNNQLLAGGHAKEVIGKEISVVPNRALDASISPVYL 60
Db 1 MMTLSGALCFRMDKDALKVLTLHNNQLLAGGHAKEVIGKEISVVPNRALDASISPVYL 60
Oy 61 GVGGSGQLSCGTEKGPILKEPVNIMELYGAKSKSFYFRDMGLTSSPESAAYPGW 120
Db 61 GVGGSGQLSCGTEKGPILKEPVNIMELYGAKSKSFYFRDMGLTSSPESAAYPGW 120
Oy 121 FLCTSPADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
Db 121 FLCTSPADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 8
US-10-948-920-2
; Sequence 2, Application US/10948920
; Publication No. US20050058625A1
; GENERAL INFORMATION:
; APPLICANT: Sime, John E.
; TITLE OF INVENTION: IL-1 DELTA DNA AND POLYPEPTIDES
; FILE REFERENCE: 0315-C
; CURRENT APPLICATION NUMBER: US/10/948,920
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US/09/965,640
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/612,921
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-948-920-2

Query Match 100.0%; Score 156; DB 5; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.4e-145;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 61 GVGGSGQLSCGTEKGPILKEPVNIMELYGAKSKSFYFRDMGLTSSPESAAYPGW 120
Db 61 GVGGSGQLSCGTEKGPILKEPVNIMELYGAKSKSFYFRDMGLTSSPESAAYPGW 120
Oy 121 FLCTSPADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
Db 121 FLCTSPADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 9
US-10-042-865-123
; Sequence 123, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: zerhusen, Bryan D
; APPLICANT: Caeman, Stacie J
; APPLICANT: Shenoy, Sureeh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangoli, Neha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Verneet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Groese, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellemann, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Utiel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-042-865-123

Query Match 99.4%; Score 155; DB 4; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.2e-144;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 MMTLSGALCFRMDKDALKVLTLHNNQLLAGGHAKEVIGKEISVVPNRALDASISPVILG 61
Db 1 MMTLSGALCFRMDKDALKVLTLHNNQLLAGGHAKEVIGKEISVVPNRALDASISPVILG 60

QY 62 VGGSGCLSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 121
DB 61 VGGSGCLSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 120
QY 122 LCTSPADQPVRLTQIPEDPAMDAPITDFFYQOCD 156
DB 121 LCTSPADQPVRLTQIPEDPAMDAPITDFFYQOCD 155

RESULT 10
US-09-775-046-11
; Sequence 11, Application US/09775046
; Patent No. US20020102234A1
; GENERAL INFORMATION:
; APPLICANT: Debets, Johannes Eduard Maria Antonius
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01073K
; CURRENT APPLICATION NUMBER: US/09/775,046
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/179,638
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-775-046-11

Query Match 98.7%; Score 154; DB 3; Length 154;
Best Local Similarity 100.0%; Pred. No. 5e-143;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSGALCFRMDKALKLYLHNNQLAGLHAENVYIGBEISVVPNRALDASLSPVILGV 62
DB 1 VLSGALCFRMDKALKLYLHNNQLAGLHAENVYIGBEISVVPNRALDASLSPVILGV 60
QY 63 QGSGSCLSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 122
DB 61 QGSGSCLSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 120
QY 123 CTSPEADQPVRLTQIPEDPAMDAPITDFFYQOCD 156
DB 121 CTSPEADQPVRLTQIPEDPAMDAPITDFFYQOCD 154

RESULT 11
US-09-730-617-55
; Sequence 55, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Suchitdas K
; APPLICANT: Shinketsu, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zethusen, Bryan D
; APPLICANT: Mezei, Peter S
; TITLE OF INVENTION: No. US20020068279A1 Proteins and Nucleic Acids Encoding the Same
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730,617
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10

; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 55
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-730-617-55

Query Match 93.6%; Score 146; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.5e-135;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CFRMDKALKLYLHNNQLAGLHAENVYIGBEISVVPNRALDASLSPVILGVGGSG 68
DB 1 CFRMDKALKLYLHNNQLAGLHAENVYIGBEISVVPNRALDASLSPVILGVGGSG 60
QY 69 LSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWFLCTSPEA 128
DB 61 LSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWFLCTSPEA 120
QY 129 DQPVRLTQIPEDPAMDAPITDFFYQO 154
DB 121 DQPVRLTQIPEDPAMDAPITDFFYQO 146

RESULT 12
US-10-205-821-1
; Sequence 1, Application US/10205821
; Publication No. US20030099650A1
; GENERAL INFORMATION:
; APPLICANT: Ho et al.
; TITLE OF INVENTION: Treatment of Immune Disorders and B Cell Disorders
; FILE REFERENCE: 28110/78645
; CURRENT APPLICATION NUMBER: US/10/205,821
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-821-1

Query Match 28.2%; Score 44; DB 4; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.1e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 LEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWFLCT 124
DB 5 LEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWFLCT 48

RESULT 13
US-10-287-190-70
; Sequence 70, Application US/10287190
; Publication No. US20040038230A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P. et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND MET
; FILE REFERENCE: 21402-780B
; CURRENT APPLICATION NUMBER: US/10/287,190
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 09/996,015
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/338626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/373806
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/338196
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/333912

```
/ PRIOR FILING DATE: 2001-11-28
/ PRIOR APPLICATION NUMBER: 60/381043
/ PRIOR FILING DATE: 2002-05-16
/ PRIOR APPLICATION NUMBER: 60/401593
/ PRIOR FILING DATE: 2002-08-07
/ PRIOR APPLICATION NUMBER: 60/334300
/ PRIOR FILING DATE: 2001-11-29
/ NUMBER OF SEQ ID NOS: 194
/ SOFTWARE: CuraSeqList version 0.1
/ SEQ ID NO 70
/ LENGTH: 143
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-287-190-70
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```
Query Match      28.2%; Score 44; DB 4; Length 143;
Best Local Similarity 100.0%; Pred.No. 6.7e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      81 LEPVNIMELYLGAKEKSKSFTFYRDMGLTSSPESAAYPGWFLCT 124
      |||
DB      75 LEPVNIMELYLGAKEKSKSFTFYRDMGLTSSPESAAYPGWFLCT 118
```

```
RESULT 14
US-10-287-190-76
/ Sequence 76, Application US/10287190
/ Publication No. US20040038230A1
/ GENERAL INFORMATION:
```

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/ APPLICANT: Alsbodtrock II, John P. et al.
/ TITLE OF INVENTION: THEAPAPUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
/ FILE REFERENCE: 21402-780B
/ CURRENT APPLICATION NUMBER: US/10/287,190
/ PRIOR FILING DATE: 2003-04-02
/ PRIOR APPLICATION NUMBER: 09/996,015
/ PRIOR FILING DATE: 2001-11-28
/ PRIOR APPLICATION NUMBER: 60/338626
/ PRIOR FILING DATE: 2001-11-05
/ PRIOR APPLICATION NUMBER: 60/373806
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: 60/338196
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/333912
/ PRIOR FILING DATE: 2001-11-28
/ PRIOR APPLICATION NUMBER: 60/381043
/ PRIOR FILING DATE: 2002-05-16
/ PRIOR APPLICATION NUMBER: 60/401593
/ PRIOR FILING DATE: 2002-08-07
/ PRIOR APPLICATION NUMBER: 60/334300
/ PRIOR FILING DATE: 2001-11-29
/ NUMBER OF SEQ ID NOS: 194
/ SOFTWARE: CuraSeqList version 0.1
/ SEQ ID NO 76
/ LENGTH: 143
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-287-190-76
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Query Match      28.2%; Score 44; DB 4; Length 143;
Best Local Similarity 100.0%; Pred.No. 6.7e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      81 LEPVNIMELYLGAKEKSKSFTFYRDMGLTSSPESAAYPGWFLCT 124
      |||
DB      75 LEPVNIMELYLGAKEKSKSFTFYRDMGLTSSPESAAYPGWFLCT 118
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RESULT 15
US-09-730-617-58
/ Sequence 58, Application US/09730617
/ Patent No. US20020068279A1
/ GENERAL INFORMATION:
/ APPLICANT: Burgees, Catherine E
```

```
/ APPLICANT: Prayaga, Sudhirdas K
/ APPLICANT: Shinkels, Richard A
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Zehnusen, Bryan D
/ APPLICANT: Mezes, Peter S
/ TITLE OF INVENTION: No. US20020068279A1el Proteins and Nucleic Acids Encoding the S
/ FILE REFERENCE: 15966-609
/ CURRENT APPLICATION NUMBER: US/09/730,617
/ PRIOR FILING DATE: 2000-12-05
/ PRIOR APPLICATION NUMBER: 60/169,056
/ PRIOR FILING DATE: 1999-12-06
/ PRIOR APPLICATION NUMBER: 60/169,886
/ PRIOR FILING DATE: 1999-12-09
/ PRIOR APPLICATION NUMBER: 60/169,866
/ PRIOR FILING DATE: 1999-12-09
/ PRIOR APPLICATION NUMBER: 60/170,252
/ PRIOR FILING DATE: 1999-12-10
/ PRIOR APPLICATION NUMBER: 60/175,740
/ PRIOR FILING DATE: 2000-01-12
/ NUMBER OF SEQ ID NOS: 100
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 58
/ LENGTH: 146
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-730-617-58
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Query Match      28.2%; Score 44; DB 3; Length 146;
Best Local Similarity 100.0%; Pred.No. 6.9e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      81 LEPVNIMELYLGAKEKSKSFTFYRDMGLTSSPESAAYPGWFLCT 124
      |||
DB      73 LEPVNIMELYLGAKEKSKSFTFYRDMGLTSSPESAAYPGWFLCT 116
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Job time : 45 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 5, 2006, 15:12:38 ; Search time 12 Seconds
(without alignments)
405.496 Million cell updates/sec

Title: US-09-770-528-2

Perfect score: 156

Sequence: 1 MMTLSGALCTRMKDSALKVL.....IPEDPANDAPITDTPFOOCD 156

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 184161 seqs, 31191982 residues

Word size : 8

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA New:*
1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB pep.*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB pep.*
4: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB pep.*
5: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB pep.*
6: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB pep.*
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8: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------------|-------------------|
| 1 | 44 | 28.2 | 155 | US-10-063-703-152 | Sequence 152, App |
| 2 | 44 | 28.2 | 155 | US-11-102-240-152 | Sequence 152, App |
| 3 | 44 | 28.2 | 155 | US-11-103-195-152 | Sequence 152, App |
| 4 | 44 | 28.2 | 155 | US-11-103-195-152 | Sequence 152, App |
| 5 | 8 | 5.1 | 206 | US-11-096-568A-11327 | Sequence 11327, A |
| 6 | 8 | 5.1 | 206 | US-11-096-568A-11327 | Sequence 11327, A |
| 7 | 8 | 5.1 | 262 | US-11-096-568A-11327 | Sequence 11327, A |
| 8 | 8 | 5.1 | 262 | US-11-096-568A-11327 | Sequence 11327, A |
| 9 | 8 | 5.1 | 308 | US-11-096-568A-11326 | Sequence 11326, A |
| 10 | 8 | 5.1 | 335 | US-11-096-568A-11325 | Sequence 11325, A |
| 11 | 8 | 5.1 | 660 | US-10-131-826A-350 | Sequence 350, App |
| 12 | 8 | 5.1 | 660 | US-10-973-115B-350 | Sequence 350, App |

ALIGNMENTS

RESULT 1
US-10-063-703-152

; Sequence 152, Application US/10063703
; Publication No. US2006008901A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,703
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 152
LENGTH: 155
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-703-152

Query Match 28.2%; Score 44; DB 6; Length 155;
Best Local Similarity 100.0%; Pred. No. 7.6e-40;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 LEPVIMELYLGAKESSFTFYRRDGLTSSPESAAYPGMFLCT 124
DB 80 LEPVIMELYLGAKESSFTFYRRDGLTSSPESAAYPGMFLCT 123

RESULT 2
US-11-102-240-152

; Sequence 152, Application US/11102240
; Publication No. US20050260647A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXP
FILE REFERENCE: P3230R1C106C
CURRENT APPLICATION NUMBER: US/11/102,240
CURRENT FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 10/063662
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 10/006867
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 199-12-09
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 152
LENGTH: 155
TYPE: PRT
ORGANISM: Homo Sapien
US-11-102-240-152

Query Match 28.2%; Score 44; DB 7; Length 155;
Best Local Similarity 100.0%; Pred. No. 7.6e-40;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 LEPVIMELYLGAKESSFTFYRRDGLTSSPESAAYPGMFLCT 124
DB 80 LEPVIMELYLGAKESSFTFYRRDGLTSSPESAAYPGMFLCT 123

RESULT 3
US-11-103-195-152

; Sequence 152, Application US/11103195
; Publication No. US20060051779A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey

```

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guirney, Austin L.
; APPLICANT: Wood, William L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230C166C1
; CURRENT APPLICATION NUMBER: US/11/103,195
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: 10/063743
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 152
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-103-195-152

Query Match          28.2%; Score 44; DB 7; Length 155;
Best Local Similarity 100.0%; Pred. No. 7,6e-40;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 LEPVNIMELYLGAKESKSTFYRRDGLTSSPESAAYPGMFLCT 124
DB 80 LEPVNIMELYLGAKESKSTFYRRDGLTSSPESAAYPGMFLCT 123

RESULT 4
US-11-169-013-1
; Sequence 1, Application US/11/169013
; Publication No. US20050244971A1
; GENERAL INFORMATION:
; APPLICANT: Korea Kumho Petrochemical Co., Ltd.
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH ENHANCED STRESS TOLERANCE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/169,013
; CURRENT FILING DATE: 2005-06-29
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 1
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-169-013-1

Query Match          5.8%; Score 9; DB 7; Length 454;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ALDASLSPV 58
DB 346 ALDASLSPV 354

RESULT 5
US-11-096-568A-11327
; Sequence 11327, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01

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; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11327
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(206)
; OTHER INFORMATION: Ceres Seq. ID no. 13598556
US-11-096-568A-11327

Query Match          5.1%; Score 8; DB 7; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LLAGGLHA 34
DB 152 LLAGGLHA 159

RESULT 6
US-11-096-568A-17757
; Sequence 17757, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17757
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(234)
; OTHER INFORMATION: Ceres Seq. ID no. 12360574
US-11-096-568A-17757

Query Match          5.1%; Score 8; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LLAGGLHA 34
DB 180 LLAGGLHA 187

RESULT 7
US-11-096-568A-17756
; Sequence 17756, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17756
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(262)
; OTHER INFORMATION: Ceres Seq. ID no. 12360573
US-11-096-568A-17756

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Query Match 5.1%; Score 8; DB 7; Length 262;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LLAGGLHA 34
|||||||
Db 208 LLAGGLHA 215

RESULT 8

US-11-096-568A-11326
; Sequence 11326, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Theryby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11326
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(264)
; OTHER INFORMATION: Ceres Seq. ID no. 13598555
US-11-096-568A-11326

Query Match 5.1%; Score 8; DB 7; Length 264;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LLAGGLHA 34
|||||||
Db 210 LLAGGLHA 217

RESULT 9

US-11-096-568A-17755
; Sequence 17755, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Theryby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17755
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(308)
; OTHER INFORMATION: Ceres Seq. ID no. 12360572
US-11-096-568A-17755

Query Match 5.1%; Score 8; DB 7; Length 308;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LLAGGLHA 34
|||||||
Db 254 LLAGGLHA 261

RESULT 10

US-11-096-568A-11325

; Sequence 11325, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Theryby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11325
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(335)
; OTHER INFORMATION: Ceres Seq. ID no. 13598554
US-11-096-568A-11325

Query Match 5.1%; Score 8; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LLAGGLHA 34
|||||||
Db 281 LLAGGLHA 288

RESULT 11

US-10-131-826A-350
; Sequence 350, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352

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; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 350
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-350

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Query Match          5.1%; Score 8; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      19 VLYLHNNQ 26
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Db       67 VLYLHNNQ 74

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RESULT 12
US-10-973-115B-350
; Sequence 350, Application US/10973115B
; Publication No. US20060040351A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Quiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODIN
; FILE REFERENCE: 39870-3330R1C300C1
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 10/973,115B
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 10/028,072
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/581,742
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: PCT/US00/05746
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/135,736
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/123,090
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 350
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-973-115B-350

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Query Match          5.1%; Score 8; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      19 VLYLHNNQ 26

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Db       67 VLYLHNNQ 74
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Search completed: April 5, 2006, 15:12:57
Job time : 13 secs

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